

SEQUENCE LISTING

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<120> Process and Materials for Production of Glucosamine and N-Acetylc
 Glucosamine

<130> 3161-18-2

<150> 60/393,348

<151> 2002-07-01

<160> 137

<170> PatentIn version 3.1

<210> 1

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<222> (1)..(1830)

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Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
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Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
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His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
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Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu	
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Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
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His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
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Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
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Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
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Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
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His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
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Glu

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Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
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cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa 240
His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
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Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu	
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gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat	672
Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp	
210 215 220	
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa	720
Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln	
225 230 235 240	
tat gac gcg ggc gat aaa ggc att tac tgt cac tac atg cag aaa gag	768
Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu	
245 250 255	
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc	816
Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile	
260 265 270	
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa	864
Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu	
275 280 285	
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct	912
Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser	
290 295 300	
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt	960
Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly	
305 310 315 320	

att ccg tgc gac gtc gaa atc gcc tcc gaa ttc cgc tat cgc aaa tct Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser	1008
325 330 335	
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu	1056
340 345 350	
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr	1104
355 360 365	
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg	1152
370 375 380	
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385 390 395 400	
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu	1248
405 410 415	
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His	1296
420 425 430	
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met	1344
435 440 445	
ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp	1392
450 455 460	
aaa cat cac gcg ctg ttc ctg agc cgt ggc gat cag tac cca atc gcg Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala	1440
465 470 475 480	
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu	1488
485 490 495	
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp	1536
500 505 510	
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu	1584
515 520 525	
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu	1632
530 535 540	
tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met	1680
545 550 555 560	

cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc	1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe	
565 570 575	
tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa	1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys	
580 585 590	
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt	1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val	
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gag taa	1830
Glu	

<210> 6
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Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
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Gly Leu Ala Val Val Asp Thr Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
 145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
 165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
 180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
 195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
 210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
 225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Cys His Tyr Met Gln Lys Glu
 245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
 260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
 275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
 290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
 305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
 325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
 340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
 355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
 370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

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 ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
 Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
 20 25 30
 ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144
 Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
 35 40 45
 ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192
 Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60
 cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa 240
 His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80
 cct tca gaa gtg aat gcg cat ccg cat gtt tcc gaa cac att gtg gtg 288
 Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95
 gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta 336
 Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
 100 105 110
 aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att 384
 Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
 115 120 125
 gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag 432
 Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
 130 135 140
 gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg 480
 Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
 145 150 155 160
 atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt 528
 Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
 165 170 175
 agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct 576
 Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
 180 185 190

gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu 195 200 205	624
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp 210 215 220	672
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln 225 230 235 240	720
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu 245 250 255	768
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile 260 265 270	816
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tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly 305 310 315 320	960
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gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu 405 410 415	1248
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ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp 450 455 460	1392
aaa cat cac gcg ccg ttc ctg ggc cgt ggc gat cag tac cca atc gcg Lys His His Ala Pro Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala 465 470 475 480	1440
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu 485 490 495	1488
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp 500 505 510	1536
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu 515 520 525	1584
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu 530 535 540	1632
tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met 545 550 555 560	1680
cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe 565 570 575	1728
tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys 580 585 590	1776
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val 595 600 605	1824
gag taa Glu	1830

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Met Cys Gly Ile Val Gly Ala Ile Ala Gln Arg Asp Val Ala Glu Ile
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Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
 35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
 100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
 115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
 130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
 145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
 165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
 180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
 195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
 210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
 225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
 245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
 260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
 275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
 290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
 305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
 325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
 340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
 355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
 370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
 385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
 405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
 420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
 435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
 450 455 460

Lys His His Ala Pro Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
 465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
 485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

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Glu

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Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
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ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192
Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu 65 70 75 80	240
cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val 85 90 95	288
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gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu 195 200 205	624
gag ggc gat att gcg gaa atc act cgc cgt tgc gta aac atc ttc gat Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp 210 215 220	672
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln 225 230 235 240	720
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu 245 250 255	768
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile 260 265 270	816
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu 275 280 285	864
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ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg 370 375 380	1152
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gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu 405 410 415	1248
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His 420 425 430	1296
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met 435 440 445	1344
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gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu 515 520 525	1584
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu 530 535 540	1632

tat	gtc	ttc	gcc	gat	cag	gat	gcg	ggt	ttt	gta	agt	agc	gat	aac	atg	1680
Tyr	Val	Phe	Ala	Asp	Gln	Asp	Ala	Gly	Phe	Val	Ser	Ser	Asp	Asn	Met	
545					550					555					560	

tac	acc	gtt	cgc	ctg	cag	ctg	ctg	gct	tac	cat	gtc	gcg	ctg	atc	aaa	1776
Tyr	Thr	Val	Pro	Leu	Gln	Leu	Leu	Ala	Tyr	His	Val	Ala	Leu	Ile	Lys	
			580					585					590			

gag taa 1830
Glu

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165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
370 375 380

Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
435 440 445

Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
450 455 460

Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

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 ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
 Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
 20 25 30
 ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144
 Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
 35 40 45
 ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg 192
 Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
 50 55 60
 cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaà 240
 His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
 65 70 75 80
 cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg 288
 Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
 85 90 95
 gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta 336
 Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
 100 105 110
 aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att 384
 Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
 115 120 125
 gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag 432
 Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
 130 135 140
 gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg 480
 Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
 145 150 155 160
 atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt 528
 Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
 165 170 175

agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser 180 185 190	576
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu 195 200 205	624
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp 210 215 220	672
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln 225 230 235 240	720
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu 245 250 255	768
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile 260 265 270	816
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu 275 280 285	864
ctg ctg tcg aag gtt gag cat att cag atc ctc gcc tgt ggt act tct Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser 290 295 300	912
tat aac tcc ggt atg gtt tcc cgc tac tgg ttt gaa tcg cta gca ggt Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly 305 310 315 320	960
att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser 325 330 335	1008
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu 340 345 350	1056
acc gcg gat acc ctg gct ggc ctg cgt ctg tcg aaa gag ctg ggt tac Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr 355 360 365	1104
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg 370 375 380	1152
gaa tcc gat ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val 385 390 395 400	1200
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu 405 410 415	1248

gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat	1296
Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His	
420 425 430	
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg	1344
Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met	
435 440 445	
ctg tct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac	1392
Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp	
450 455 460	
aaa cat cac gcg ctg ttc ctg agc cgt ggc gat cag tac cca atc gcg	1440
Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala	
465 470 475 480	
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa	1488
Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu	
485 490 495	
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat	1536
Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp	
500 505 510	
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gaa ttg ctg gaa	1584
Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu	
515 520 525	
aaa ctg aaa tcc aac att gaa gaa gtt cgc gcg cgt ggc ggt cag ttg	1632
Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu	
530 535 540	
tat gtc ttc gcc gat cag gat gcg ggt ttt gta agt agc gat aac atg	1680
Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met	
545 550 555 560	
cac atc atc gag atg ccg cat gtg gaa gag gtg att gca ccg atc ttc	1728
His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe	
565 570 575	
tac acc gtt ccg ctg cag ctg ctg gct tac cat gtc gcg ctg atc aaa	1776
Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys	
580 585 590	
ggc acc gac gtt gac cag ccg cgt aac ctg gca aaa tcg gtt acg gtt	1824
Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val	
595 600 605	
gag taa	1830
Glu	

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Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
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Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu
50 55 60

His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu
65 70 75 80

Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val
85 90 95

Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu
100 105 110

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
 245 250 255
 Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
 260 265 270
 Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
 275 280 285
 Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
 290 295 300
 Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
 305 310 315 320
 Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
 325 330 335
 Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
 340 345 350
 Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
 355 360 365
 Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
 370 375 380
 Glu Ser Asp Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
 385 390 395 400
 Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
 405 410 415
 Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
 420 425 430
 Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
 435 440 445
 Leu Ser Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
 450 455 460
 Lys His His Ala Leu Phe Leu Ser Arg Gly Asp Gln Tyr Pro Ile Ala
 465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Glu Leu Leu Glu
515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
580 585 590

Gly Thr Asp Val Asp Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val
595 600 605

Glu

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ctt ctt gaa ggt tta cgt cgt ctg gaa tac cgc gga tat gac tct gcc 96
Leu Leu Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr Asp Ser Ala
20 25 30

ggt ctg gcc gtt gtt gat gca gaa ggt cat atg acc cgc ctg cgt cgc 144
Gly Leu Ala Val Val Asp Ala Glu Gly His Met Thr Arg Leu Arg Arg
35 40 45

ctc ggt aaa gtc cag atg ctg gca cag gca gcg gaa gaa cat cct ctg Leu Gly Lys Val Gln Met Leu Ala Gln Ala Ala Glu Glu His Pro Leu 50 55 60	192
cat ggc ggc act ggt att gct cac act cgc tgg gcg acc cac ggt gaa His Gly Gly Thr Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Glu 65 70 75 80	240
cct tca gaa gtg aat gcg cat ccg cat gtt tct gaa cac att gtg gtg Pro Ser Glu Val Asn Ala His Pro His Val Ser Glu His Ile Val Val 85 90 95	288
gtg cat aac ggc atc atc gaa aac cat gaa ccg ctg cgt gaa gag cta Val His Asn Gly Ile Ile Glu Asn His Glu Pro Leu Arg Glu Glu Leu 100 105 110	336
aaa gcg cgt ggc tat acc ttc gtt tct gaa acc gac acc gaa gtg att Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile 115 120 125	384
gcc cat ctg gtg aac tgg gag ctg aaa caa ggc ggg act ctg cgt gag Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu 130 135 140	432
gcc gtt ctg cgt gct atc ccg cag ctg cgt ggt gcg tac ggt aca gtg Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val 145 150 155 160	480
atc atg gac tcc cgt cac ccg gat acc ctg ctg gcg gca cgt tct ggt Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly 165 170 175	528
agt ccg ctg gtg att ggc ctg ggg atg ggc gaa aac ttt atc gct tct Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser 180 185 190	576
gac cag ctg gcg ctg ttg ccg gtg acc cgt cgc ttt atc ttc ctt gaa Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu 195 200 205	624
gag ggc gat att gcg gaa atc act cgc cgt tcg gta aac atc ttc gat Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp 210 215 220	672
aaa act ggc gcg gaa gta aaa cgt cag gat atc gaa tcc aat ctg caa Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln 225 230 235 240	720
tat gac gcg ggc gat aaa ggc att tac cgt cac tac atg cag aaa gag Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu 245 250 255	768
atc tac gaa cag ccg aac gcg atc aaa aac acc ctt acc gga cgc atc Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile 260 265 270	816
agc cac ggt cag gtt gat tta agc gag ctg gga ccg aac gcc gac gaa Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu 275 280 285	864

ctg ctg tgc aag gtt gag cat att cag atc ctc gcc tgt ggt act tct Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser 290 295 300	912
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att ccg tgc gac gtc gaa atc gcc tct gaa ttc cgc tat cgc aaa tct Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser 325 330 335	1008
gcc gtg cgt cgt aac agc ctg atg atc acc ttg tca cag tct ggc gaa Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu 340 345 350	1056
acc gcg gat acc ctg gct ggc ctg cgt ctg tgc aaa gag ctg ggt tac Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr 355 360 365	1104
ctt ggt tca ctg gca atc tgt aac gtt ccg ggt tct tct ctg gtg cgc Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg 370 375 380	1152
gaa tcc gtt ctg gcg cta atg acc aac gcg ggt aca gaa atc ggc gtg Glu Ser Val Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val 385 390 395 400	1200
gca tcc act aaa gca ttc acc act cag tta act gtg ctg ttg atg ctg Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu 405 410 415	1248
gtg gcg aag ctg tct cgc ctg aaa ggt ctg gat gcc tcc att gaa cat Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His 420 425 430	1296
gac atc gtg cat ggt ctg cag gcg ctg ccg agc cgt att gag cag atg Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met 435 440 445	1344
ctg cct cag gac aaa cgc att gaa gcg ctg gca gaa gat ttc tct gac Leu Pro Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp 450 455 460	1392
aaa cat cac gcg ctg ttc ctg ggc cgt ggc gat cag tac cca atc gcg Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala 465 470 475 480	1440
ctg gaa ggc gca ttg aag ttg aaa gag atc tct tac att cac gct gaa Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu 485 490 495	1488
gcc tac gct gct ggc gaa ctg aaa cac ggt ccg ctg gcg cta att gat Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp 500 505 510	1536
gcc gat atg ccg gtt att gtt gtt gca ccg aac aac gga ttg ctg gaa Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Gly Leu Leu Glu 515 520 525	1584

aaa	ctg	aaa	tcc	aac	att	gaa	gaa	gtt	cgc	gcg	cgt	ggc	ggg	cag	ttg	1632
Lys	Leu	Lys	Ser	Asn	Ile	Glu	Glu	Val	Arg	Ala	Arg	Gly	Gly	Gln	Leu	
	530					535					540					

tat	gtc	ttc	gcc	gat	cag	gat	gcg	ggg	ttt	gta	agt	agc	gat	aac	atg	1680
Tyr	Val	Phe	Ala	Asp	Gln	Asp	Ala	Gly	Phe	Val	Ser	Ser	Asp	Asn	Met	
	545				550				555						560	

cac	atc	atc	gag	atg	ccg	cat	gtg	gaa	gag	gtg	att	gca	ccg	atc	ttc	1728
His	Ile	Ile	Glu	Met	Pro	His	Val	Glu	Glu	Val	Ile	Ala	Pro	Ile	Phe	
			565					570						575		

tac	acc	gtt	ccg	ctg	cag	ctg	ctg	gct	tac	cat	gtc	gcg	ctg	atc	aaa	1776
Tyr	Thr	Val	Pro	Leu	Gln	Leu	Leu	Ala	Tyr	His	Val	Ala	Leu	Ile	Lys	
			580					585					590			

ggc	acc	gac	gtt	gac	cag	ccg	cgt	aac	ctg	gca	aaa	tcg	gtt	acg	gtt	1824
Gly	Thr	Asp	Val	Asp	Gln	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	
		595					600					605				

gag	taa															1830
Glu																

<210> 14
 <211> 609
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<400> 14

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			20					25					30		

Gly	Leu	Ala	Val	Val	Asp	Ala	Glu	Gly	His	Met	Thr	Arg	Leu	Arg	Arg
		35					40					45			

Leu	Gly	Lys	Val	Gln	Met	Leu	Ala	Gln	Ala	Ala	Glu	Glu	His	Pro	Leu
	50					55					60				

His	Gly	Gly	Thr	Gly	Ile	Ala	His	Thr	Arg	Trp	Ala	Thr	His	Gly	Glu
65					70				75					80	

Pro	Ser	Glu	Val	Asn	Ala	His	Pro	His	Val	Ser	Glu	His	Ile	Val	Val
				85					90					95	

Val	His	Asn	Gly	Ile	Ile	Glu	Asn	His	Glu	Pro	Leu	Arg	Glu	Glu	Leu
			100					105					110		

Lys Ala Arg Gly Tyr Thr Phe Val Ser Glu Thr Asp Thr Glu Val Ile
 115 120 125

Ala His Leu Val Asn Trp Glu Leu Lys Gln Gly Gly Thr Leu Arg Glu
 130 135 140

Ala Val Leu Arg Ala Ile Pro Gln Leu Arg Gly Ala Tyr Gly Thr Val
 145 150 155 160

Ile Met Asp Ser Arg His Pro Asp Thr Leu Leu Ala Ala Arg Ser Gly
 165 170 175

Ser Pro Leu Val Ile Gly Leu Gly Met Gly Glu Asn Phe Ile Ala Ser
 180 185 190

Asp Gln Leu Ala Leu Leu Pro Val Thr Arg Arg Phe Ile Phe Leu Glu
 195 200 205

Glu Gly Asp Ile Ala Glu Ile Thr Arg Arg Ser Val Asn Ile Phe Asp
 210 215 220

Lys Thr Gly Ala Glu Val Lys Arg Gln Asp Ile Glu Ser Asn Leu Gln
 225 230 235 240

Tyr Asp Ala Gly Asp Lys Gly Ile Tyr Arg His Tyr Met Gln Lys Glu
 245 250 255

Ile Tyr Glu Gln Pro Asn Ala Ile Lys Asn Thr Leu Thr Gly Arg Ile
 260 265 270

Ser His Gly Gln Val Asp Leu Ser Glu Leu Gly Pro Asn Ala Asp Glu
 275 280 285

Leu Leu Ser Lys Val Glu His Ile Gln Ile Leu Ala Cys Gly Thr Ser
 290 295 300

Tyr Asn Ser Gly Met Val Ser Arg Tyr Trp Phe Glu Ser Leu Ala Gly
 305 310 315 320

Ile Pro Cys Asp Val Glu Ile Ala Ser Glu Phe Arg Tyr Arg Lys Ser
 325 330 335

Ala Val Arg Arg Asn Ser Leu Met Ile Thr Leu Ser Gln Ser Gly Glu
 340 345 350

Thr Ala Asp Thr Leu Ala Gly Leu Arg Leu Ser Lys Glu Leu Gly Tyr
 355 360 365

Leu Gly Ser Leu Ala Ile Cys Asn Val Pro Gly Ser Ser Leu Val Arg
 370 375 380

Glu Ser Val Leu Ala Leu Met Thr Asn Ala Gly Thr Glu Ile Gly Val
 385 390 395 400

Ala Ser Thr Lys Ala Phe Thr Thr Gln Leu Thr Val Leu Leu Met Leu
 405 410 415

Val Ala Lys Leu Ser Arg Leu Lys Gly Leu Asp Ala Ser Ile Glu His
 420 425 430

Asp Ile Val His Gly Leu Gln Ala Leu Pro Ser Arg Ile Glu Gln Met
 435 440 445

Leu Pro Gln Asp Lys Arg Ile Glu Ala Leu Ala Glu Asp Phe Ser Asp
 450 455 460

Lys His His Ala Leu Phe Leu Gly Arg Gly Asp Gln Tyr Pro Ile Ala
 465 470 475 480

Leu Glu Gly Ala Leu Lys Leu Lys Glu Ile Ser Tyr Ile His Ala Glu
 485 490 495

Ala Tyr Ala Ala Gly Glu Leu Lys His Gly Pro Leu Ala Leu Ile Asp
 500 505 510

Ala Asp Met Pro Val Ile Val Val Ala Pro Asn Asn Gly Leu Leu Glu
 515 520 525

Lys Leu Lys Ser Asn Ile Glu Glu Val Arg Ala Arg Gly Gly Gln Leu
 530 535 540

Tyr Val Phe Ala Asp Gln Asp Ala Gly Phe Val Ser Ser Asp Asn Met
 545 550 555 560

His Ile Ile Glu Met Pro His Val Glu Glu Val Ile Ala Pro Ile Phe
 565 570 575

Tyr Thr Val Pro Leu Gln Leu Leu Ala Tyr His Val Ala Leu Ile Lys
 580 585 590

Gly	Thr	Asp	Val	Asp	Gln	Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val
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Glu

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tta tta aaa ggg tta gag aag ctt gag tat cgc ggt tat gac tct gct	96
Leu Leu Lys Gly Leu Glu Lys Leu Glu Tyr Arg Gly Tyr Asp Ser Ala	
20 25 30	
ggt att gct gtt gcc aac gaa cag gga atc cat gtg ttc aaa gaa aaa	144
Gly Ile Ala Val Ala Asn Glu Gln Gly Ile His Val Phe Lys Glu Lys	
35 40 45	
gga cgc att gca gat ctt cgt gaa gtt gtg gat gcc aat gta gaa gcg	192
Gly Arg Ile Ala Asp Leu Arg Glu Val Val Asp Ala Asn Val Glu Ala	
50 55 60	
aaa gcc gga att ggg cat act cgc tgg gcg aca cac ggc gaa cca agc	240
Lys Ala Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Glu Pro Ser	
65 70 75 80	
tat ctg aac gct cac ccg cat caa agc gca ctg ggc cgc ttt aca ctt	288
Tyr Leu Asn Ala His Pro His Gln Ser Ala Leu Gly Arg Phe Thr Leu	
85 90 95	
gtt cac aac ggc gtg atc gag aac tat gtt cag ctg aag caa gag tat	336
Val His Asn Gly Val Ile Glu Asn Tyr Val Gln Leu Lys Gln Glu Tyr	
100 105 110	
ttg caa gat gta gag ctc aaa agt gac acc gat aca gaa gta gtc gtt	384
Leu Gln Asp Val Glu Leu Lys Ser Asp Thr Asp Thr Glu Val Val Val	
115 120 125	
caa gta atc gag caa ttc gtc aat gga gga ctt gag aca gaa gaa gcg	432
Gln Val Ile Glu Gln Phe Val Asn Gly Gly Leu Glu Thr Glu Glu Ala	
130 135 140	
ttc cgc aaa aca ctt aca ctg tta aaa ggc tct tat gca att gct tta	480
Phe Arg Lys Thr Leu Thr Leu Leu Lys Gly Ser Tyr Ala Ile Ala Leu	
145 150 155 160	

ttc gat aac gac aac aga gaa acg att ttt gta gcg aaa aac aaa agc Phe Asp Asn Asp Asn Arg Glu Thr Ile Phe Val Ala Lys Asn Lys Ser 165 170 175	528
cct cta tta gta ggt ctt gga gat aca ttc aac gtc gta gca tct gat Pro Leu Leu Val Gly Leu Gly Asp Thr Phe Asn Val Val Ala Ser Asp 180 185 190	576
gcg atg gcg atg ctt caa gta acc aac gaa tac gta gag ctg atg gat Ala Met Ala Met Leu Gln Val Thr Asn Glu Tyr Val Glu Leu Met Asp 195 200 205	624
aaa gaa atg gtt atc gtc act gat gac caa gtt gtc atc aaa aac ctt Lys Glu Met Val Ile Val Thr Asp Asp Gln Val Val Ile Lys Asn Leu 210 215 220	672
gat ggt gac gtg att aca cgt gcg tct tat att gct gag ctt gat gcc Asp Gly Asp Val Ile Thr Arg Ala Ser Tyr Ile Ala Glu Leu Asp Ala 225 230 235 240	720
agt gat atc gaa aaa ggc acg tac cct cac tac atg ttg aaa gaa acg Ser Asp Ile Glu Lys Gly Thr Tyr Pro His Tyr Met Leu Lys Glu Thr 245 250 255	768
gat gag cag cct gtt gtt atg cgc aaa atc atc caa acg tat caa gat Asp Glu Gln Pro Val Val Met Arg Lys Ile Ile Gln Thr Tyr Gln Asp 260 265 270	816
gaa aac ggc aag ctg tct gtg cct ggc gat atc gct gcc gct gta gcg Glu Asn Gly Lys Leu Ser Val Pro Gly Asp Ile Ala Ala Ala Val Ala 275 280 285	864
gaa gcg gac cgc atc tat atc att ggc tgc gga aca agc tac cat gca Glu Ala Asp Arg Ile Tyr Ile Ile Gly Cys Gly Thr Ser Tyr His Ala 290 295 300	912
gga ctt gtc ggt aaa caa tat att gaa atg tgg gca aac gtg ccg gtt Gly Leu Val Gly Lys Gln Tyr Ile Glu Met Trp Ala Asn Val Pro Val 305 310 315 320	960
gaa gtg cat gta gcg agt gaa ttc tcc tac aac atg ccg ctt ctg tct Glu Val His Val Ala Ser Glu Phe Ser Tyr Asn Met Pro Leu Leu Ser 325 330 335	1008
aag aaa ccg ctc ttc att ttc ctt tct caa agc gga gaa aca gca gac Lys Lys Pro Leu Phe Ile Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp 340 345 350	1056
agc cgc gcg gta ctc gtt caa gtc aaa gcg ctc gga cac aaa gcc ctg Ser Arg Ala Val Leu Val Gln Val Lys Ala Leu Gly His Lys Ala Leu 355 360 365	1104
aca atc aca aac gta cct gga tca acg ctt tct cgt gaa gct gac tat Thr Ile Thr Asn Val Pro Gly Ser Thr Leu Ser Arg Glu Ala Asp Tyr 370 375 380	1152
aca ttg ctg ctt cat gca ggc cct gag atc gct gtt gcg tca acg aaa Thr Leu Leu Leu His Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys 385 390 395 400	1200

gca tac act gca caa atc gca gtt ctg gcg gtt ctt gct tct gtg gct Ala Tyr Thr Ala Gln Ile Ala Val Leu Ala Val Leu Ala Ser Val Ala 405 410 415	1248
gct gac aaa aat ggc atc aat atc gga ttt gac ctc gtc aaa gaa ctc Ala Asp Lys Asn Gly Ile Asn Ile Gly Phe Asp Leu Val Lys Glu Leu 420 425 430	1296
ggc atc gct gca aac gca atg gaa gct cta tgc gac cag aaa gac gaa Gly Ile Ala Ala Asn Ala Met Glu Ala Leu Cys Asp Gln Lys Asp Glu 435 440 445	1344
atg gaa atg atc gct cgt gaa tac ctg act gta tcc aga aat gct ttc Met Glu Met Ile Ala Arg Glu Tyr Leu Thr Val Ser Arg Asn Ala Phe 450 455 460	1392
ttc atc gga cgc ggc ctt gac tac ttc gta tgt gtc gaa ggc gca ctg Phe Ile Gly Arg Gly Leu Asp Tyr Phe Val Cys Val Glu Gly Ala Leu 465 470 475 480	1440
aag ctg aaa gag att tct tac atc cag gca gaa ggt ttt gcc ggc ggt Lys Leu Lys Glu Ile Ser Tyr Ile Gln Ala Glu Gly Phe Ala Gly Gly 485 490 495	1488
gag cta aag cac gga acg att gcc ttg atc gaa caa gga aca cca gta Glu Leu Lys His Gly Thr Ile Ala Leu Ile Glu Gln Gly Thr Pro Val 500 505 510	1536
ttc gca ctg gca act caa gag cat gta aac cta agc atc cgc gga aac Phe Ala Leu Ala Thr Gln Glu His Val Asn Leu Ser Ile Arg Gly Asn 515 520 525	1584
gtc aaa gaa gtt gct gct cgc gga gca aac aca tgc atc atc tca ctg Val Lys Glu Val Ala Ala Arg Gly Ala Asn Thr Cys Ile Ile Ser Leu 530 535 540	1632
aaa ggc cta gac gat gcg gat gac aga ttc gta ttg ccg gaa gta aac Lys Gly Leu Asp Asp Ala Asp Asp Arg Phe Val Leu Pro Glu Val Asn 545 550 555 560	1680
cca gcg ctt gct ccg ttg gta tct gtt gtt cca ttg cag ctg atc gct Pro Ala Leu Ala Pro Leu Val Ser Val Val Pro Leu Gln Leu Ile Ala 565 570 575	1728
tac tat gct gca ctg cat cgc ggc tgt gat gtg gat aaa cct cgt aac Tyr Tyr Ala Ala Leu His Arg Gly Cys Asp Val Asp Lys Pro Arg Asn 580 585 590	1776
ctt gcg aag agt gtt act gtg gag taa Leu Ala Lys Ser Val Thr Val Glu 595 600	1803

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 20 25 30
 Gly Ile Ala Val Ala Asn Glu Gln Gly Ile His Val Phe Lys Glu Lys
 35 40 45
 Gly Arg Ile Ala Asp Leu Arg Glu Val Val Asp Ala Asn Val Glu Ala
 50 55 60
 Lys Ala Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Glu Pro Ser
 65 70 75 80
 Tyr Leu Asn Ala His Pro His Gln Ser Ala Leu Gly Arg Phe Thr Leu
 85 90 95
 Val His Asn Gly Val Ile Glu Asn Tyr Val Gln Leu Lys Gln Glu Tyr
 100 105 110
 Leu Gln Asp Val Glu Leu Lys Ser Asp Thr Asp Thr Glu Val Val Val
 115 120 125
 Gln Val Ile Glu Gln Phe Val Asn Gly Gly Leu Glu Thr Glu Glu Ala
 130 135 140
 Phe Arg Lys Thr Leu Thr Leu Leu Lys Gly Ser Tyr Ala Ile Ala Leu
 145 150 155 160
 Phe Asp Asn Asp Asn Arg Glu Thr Ile Phe Val Ala Lys Asn Lys Ser
 165 170 175
 Pro Leu Leu Val Gly Leu Gly Asp Thr Phe Asn Val Val Ala Ser Asp
 180 185 190
 Ala Met Ala Met Leu Gln Val Thr Asn Glu Tyr Val Glu Leu Met Asp
 195 200 205
 Lys Glu Met Val Ile Val Thr Asp Asp Gln Val Val Ile Lys Asn Leu
 210 215 220
 Asp Gly Asp Val Ile Thr Arg Ala Ser Tyr Ile Ala Glu Leu Asp Ala
 225 230 235 240

Ser Asp Ile Glu Lys Gly Thr Tyr Pro His Tyr Met Leu Lys Glu Thr
245 250 255

Asp Glu Gln Pro Val Val Met Arg Lys Ile Ile Gln Thr Tyr Gln Asp
260 265 270

Glu Asn Gly Lys Leu Ser Val Pro Gly Asp Ile Ala Ala Ala Val Ala
275 280 285

Glu Ala Asp Arg Ile Tyr Ile Ile Gly Cys Gly Thr Ser Tyr His Ala
290 295 300

Gly Leu Val Gly Lys Gln Tyr Ile Glu Met Trp Ala Asn Val Pro Val
305 310 315 320

Glu Val His Val Ala Ser Glu Phe Ser Tyr Asn Met Pro Leu Leu Ser
325 330 335

Lys Lys Pro Leu Phe Ile Phe Leu Ser Gln Ser Gly Glu Thr Ala Asp
340 345 350

Ser Arg Ala Val Leu Val Gln Val Lys Ala Leu Gly His Lys Ala Leu
355 360 365

Thr Ile Thr Asn Val Pro Gly Ser Thr Leu Ser Arg Glu Ala Asp Tyr
370 375 380

Thr Leu Leu Leu His Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys
385 390 395 400

Ala Tyr Thr Ala Gln Ile Ala Val Leu Ala Val Leu Ala Ser Val Ala
405 410 415

Ala Asp Lys Asn Gly Ile Asn Ile Gly Phe Asp Leu Val Lys Glu Leu
420 425 430

Gly Ile Ala Ala Asn Ala Met Glu Ala Leu Cys Asp Gln Lys Asp Glu
435 440 445

Met Glu Met Ile Ala Arg Glu Tyr Leu Thr Val Ser Arg Asn Ala Phe
450 455 460

Phe Ile Gly Arg Gly Leu Asp Tyr Phe Val Cys Val Glu Gly Ala Leu
465 470 475 480

Lys Leu Lys Glu Ile Ser Tyr Ile Gln Ala Glu Gly Phe Ala Gly Gly
485 490 495

Glu Leu Lys His Gly Thr Ile Ala Leu Ile Glu Gln Gly Thr Pro Val
500 505 510

Phe Ala Leu Ala Thr Gln Glu His Val Asn Leu Ser Ile Arg Gly Asn
515 520 525

Val Lys Glu Val Ala Ala Arg Gly Ala Asn Thr Cys Ile Ile Ser Leu
530 535 540

Lys Gly Leu Asp Asp Ala Asp Asp Arg Phe Val Leu Pro Glu Val Asn
545 550 555 560

Pro Ala Leu Ala Pro Leu Val Ser Val Val Pro Leu Gln Leu Ile Ala
565 570 575

Tyr Tyr Ala Ala Leu His Arg Gly Cys Asp Val Asp Lys Pro Arg Asn
580 585 590

Leu Ala Lys Ser Val Thr Val Glu
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gga gaa att atc gac acc tta gtg gat ggt tta caa aga tta gaa tat 96
Gly Glu Ile Ile Asp Thr Leu Val Asp Gly Leu Gln Arg Leu Glu Tyr
20 25 30

aga ggc tat gat tcc acc ggt att gct atc gat ggt gac gaa gct gat 144
Arg Gly Tyr Asp Ser Thr Gly Ile Ala Ile Asp Gly Asp Glu Ala Asp
35 40 45

tct act ttc atc tat aag caa atc ggt aaa gtg agt gct ttg aaa gag 192
Ser Thr Phe Ile Tyr Lys Gln Ile Gly Lys Val Ser Ala Leu Lys Glu
50 55 60

gag att act aag caa aat ccg aac aga gac gtt act ttt gtc tct cat	240
Glu Ile Thr Lys Gln Asn Pro Asn Arg Asp Val Thr Phe Val Ser His	
65 70 75 80	
tgt ggt att gcg cat act aga tgg gct act cac ggt cga cca gaa caa	288
Cys Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Arg Pro Glu Gln	
85 90 95	
ggt aac tgt cac cct caa aga tct gac cca gaa gac caa ttt gtg gtc	336
Val Asn Cys His Pro Gln Arg Ser Asp Pro Glu Asp Gln Phe Val Val	
100 105 110	
ggt cat aat ggt atc atc aca aat ttt aga gaa ctg aag act ctt tta	384
Val His Asn Gly Ile Ile Thr Asn Phe Arg Glu Leu Lys Thr Leu Leu	
115 120 125	
att aac aaa ggt tat aaa ttc gaa agt gat acc gat acc gag tgt att	432
Ile Asn Lys Gly Tyr Lys Phe Glu Ser Asp Thr Asp Thr Glu Cys Ile	
130 135 140	
gct aaa cta tat ttg cat tta tag aat aca aat tta caa aat ggg cat	480
Ala Lys Leu Tyr Leu His Leu Tyr Asn Thr Asn Leu Gln Asn Gly His	
145 150 155 160	
gac tta gat ttc cac gaa tta acc aag cta gtt ctt tta gaa cta gaa	528
Asp Leu Asp Phe His Glu Leu Thr Lys Leu Val Leu Leu Glu Leu Glu	
165 170 175	
ggt tca tac ggg tta tta tgt aaa tct tgt cac tat cct aat gag gtt	576
Gly Ser Tyr Gly Leu Leu Cys Lys Ser Cys His Tyr Pro Asn Glu Val	
180 185 190	
atc gcc act aga aaa ggg tcc cct tta ctg att ggt gtc aaa tct gaa	624
Ile Ala Thr Arg Lys Gly Ser Pro Leu Leu Ile Gly Val Lys Ser Glu	
195 200 205	
aaa aaa cta aaa gtc gac ttc gtg gat gtg gaa ttt ccc gaa gaa aac	672
Lys Lys Leu Lys Val Asp Phe Val Asp Val Glu Phe Pro Glu Glu Asn	
210 215 220	
gct ggt caa ccg gaa att cca ttg aaa tct aac aac aaa tca ttt ggc	720
Ala Gly Gln Pro Glu Ile Pro Leu Lys Ser Asn Asn Lys Ser Phe Gly	
225 230 235 240	
ttg ggc cca aag aaa gct cgt gaa ttt gaa gct ggt tcc caa aat gcc	768
Leu Gly Pro Lys Lys Ala Arg Glu Phe Glu Ala Gly Ser Gln Asn Ala	
245 250 255	
aat tta cta cca att gcc gcc aat gaa ttt aac ttg aga cat tct caa	816
Asn Leu Leu Pro Ile Ala Ala Asn Glu Phe Asn Leu Arg His Ser Gln	
260 265 270	
tcc agg gct ttc cta tca gaa gat gga tct cca aca ccg gtg gaa ttt	864
Ser Arg Ala Phe Leu Ser Glu Asp Gly Ser Pro Thr Pro Val Glu Phe	
275 280 285	
ttt gtt tct tcg gat gcg gca tct gtt gtt aaa cat acc aag aag gtg	912
Phe Val Ser Ser Asp Ala Ala Ser Val Val Lys His Thr Lys Lys Val	
290 295 300	

cta ttt tta gaa gat gac gat ttg gct cat att tac gat ggt gag tta Leu Phe Leu Glu Asp Asp Asp Leu Ala His Ile Tyr Asp Gly Glu Leu 305 310 315 320	960
cat att cat aga tct aga aga gaa gta ggc gca tca atg aca agg tcc His Ile His Arg Ser Arg Arg Glu Val Gly Ala Ser Met Thr Arg Ser 325 330 335	1008
att caa act tta gag atg gag tta gct cag atc atg aag ggc cct tac Ile Gln Thr Leu Glu Met Glu Leu Ala Gln Ile Met Lys Gly Pro Tyr 340 345 350	1056
gac cat ttt atg caa aag gaa atc tat gag caa cca gaa tct act ttc Asp His Phe Met Gln Lys Glu Ile Tyr Glu Gln Pro Glu Ser Thr Phe 355 360 365	1104
aat act atg aga ggt aga atc gac tat gaa aat aat aaa gtg ata ttg Asn Thr Met Arg Gly Arg Ile Asp Tyr Glu Asn Asn Lys Val Ile Leu 370 375 380	1152
ggg ggt tta aag gca tgg tta cca gtt gtc aga aga gca cgg aga ctg Gly Gly Leu Lys Ala Trp Leu Pro Val Val Arg Arg Ala Arg Arg Leu 385 390 395 400	1200
atc atg atc gca tgc ggt act tct tat cat tca tgt ttg gct act cgt Ile Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg 405 410 415	1248
gct atc ttc gaa gaa tta tca gat atc cca gtt agt gtg gaa tta gcg Ala Ile Phe Glu Glu Leu Ser Asp Ile Pro Val Ser Val Glu Leu Ala 420 425 430	1296
tct gac ttt ctg gac aga aaa tgc cct gtc ttc aga gac gat gta tgc Ser Asp Phe Leu Asp Arg Lys Cys Pro Val Phe Arg Asp Asp Val Cys 435 440 445	1344
gtg ttt gtt tca caa agt ggt gaa act gcg gat acc atg ctg gct cta Val Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Thr Met Leu Ala Leu 450 455 460	1392
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gtt ggt tct tct atc tct cgt gtc acc cac tgt ggt gtt cat att aac Val Gly Ser Ser Ile Ser Arg Val Thr His Cys Gly Val His Ile Asn 485 490 495	1488
gct ggt cct gaa att ggt gtt gcc tct aca aaa gct tat act tcc cag Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln 500 505 510	1536
tat att gcc tta gtg atg ttt gct cta tcg ctg tca gat gac cgt gta Tyr Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asp Asp Arg Val 515 520 525	1584
tcg aaa ata gac aga aga att gaa atc att caa ggc ttg aag tta atc Ser Lys Ile Asp Arg Arg Ile Glu Ile Ile Gln Gly Leu Lys Leu Ile 530 535 540	1632

ccg ggc caa att aag cag gta tta aag ctg gaa cca aga ata aaa aag	1680
Pro Gly Gln Ile Lys Gln Val Leu Lys Leu Glu Pro Arg Ile Lys Lys	
545 550 555 560	
ctc tgt gcg act gaa tta aag gat caa aaa tct cta ttg tta ttg ggt	1728
Leu Cys Ala Thr Glu Leu Lys Asp Gln Lys Ser Leu Leu Leu Leu Gly	
565 570 575	
aga ggt tac caa ttt gct gct gct ctg gaa ggt gct ttg aag atc aaa	1776
Arg Gly Tyr Gln Phe Ala Ala Ala Leu Glu Gly Ala Leu Lys Ile Lys	
580 585 590	
gaa att tct tat atg cat tct gaa ggt gtt ttg gca ggt gag ttg aag	1824
Glu Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys	
595 600 605	
cac ggt gtc ttg gcc ttg gtg gac gaa aac ttg cca atc att gct ttt	1872
His Gly Val Leu Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Ala Phe	
610 615 620	
ggg acc aga gac tct cta ttc cct aaa gta gtt tcc tct att gag caa	1920
Gly Thr Arg Asp Ser Leu Phe Pro Lys Val Val Ser Ser Ile Glu Gln	
625 630 635 640	
gtt act gca aga aag ggc cat cca att att att tgt aac gaa aat gat	1968
Val Thr Ala Arg Lys Gly His Pro Ile Ile Ile Cys Asn Glu Asn Asp	
645 650 655	
gaa gtg tgg gcg caa aaa tct aaa tca atc gac ctg caa acc tta gaa	2016
Glu Val Trp Ala Gln Lys Ser Lys Ser Ile Asp Leu Gln Thr Leu Glu	
660 665 670	
gtt cca caa act gtt gat tgt tta caa ggt cta att aat att att cca	2064
Val Pro Gln Thr Val Asp Cys Leu Gln Gly Leu Ile Asn Ile Ile Pro	
675 680 685	
tta caa cta atg tca tat tgg ttg gct gtt aat aaa ggg att gat gtt	2112
Leu Gln Leu Met Ser Tyr Trp Leu Ala Val Asn Lys Gly Ile Asp Val	
690 695 700	
gat ttt cca aga aac ttg gct aaa tct gtt acc gtc gaa taa	2154
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20 25 30

Arg Gly Tyr Asp Ser Thr Gly Ile Ala Ile Asp Gly Asp Glu Ala Asp
 35 40 45

Ser Thr Phe Ile Tyr Lys Gln Ile Gly Lys Val Ser Ala Leu Lys Glu
 50 55 60

Glu Ile Thr Lys Gln Asn Pro Asn Arg Asp Val Thr Phe Val Ser His
 65 70 75 80

Cys Gly Ile Ala His Thr Arg Trp Ala Thr His Gly Arg Pro Glu Gln
 85 90 95

Val Asn Cys His Pro Gln Arg Ser Asp Pro Glu Asp Gln Phe Val Val
 100 105 110

Val His Asn Gly Ile Ile Thr Asn Phe Arg Glu Leu Lys Thr Leu Leu
 115 120 125

Ile Asn Lys Gly Tyr Lys Phe Glu Ser Asp Thr Asp Thr Glu Cys Ile
 130 135 140

Ala Lys Leu Tyr Leu His Leu Tyr Asn Thr Asn Leu Gln Asn Gly His
 145 150 155 160

Asp Leu Asp Phe His Glu Leu Thr Lys Leu Val Leu Leu Glu Leu Glu
 165 170 175

Gly Ser Tyr Gly Leu Leu Cys Lys Ser Cys His Tyr Pro Asn Glu Val
 180 185 190

Ile Ala Thr Arg Lys Gly Ser Pro Leu Leu Ile Gly Val Lys Ser Glu
 195 200 205

Lys Lys Leu Lys Val Asp Phe Val Asp Val Glu Phe Pro Glu Glu Asn
 210 215 220

Ala Gly Gln Pro Glu Ile Pro Leu Lys Ser Asn Asn Lys Ser Phe Gly
 225 230 235 240

Leu Gly Pro Lys Lys Ala Arg Glu Phe Glu Ala Gly Ser Gln Asn Ala
 245 250 255

Asn Leu Leu Pro Ile Ala Ala Asn Glu Phe Asn Leu Arg His Ser Gln
 260 265 270

Ser Arg Ala Phe Leu Ser Glu Asp Gly Ser Pro Thr Pro Val Glu Phe
275 280 285

Phe Val Ser Ser Asp Ala Ala Ser Val Val Lys His Thr Lys Lys Val
290 295 300

Leu Phe Leu Glu Asp Asp Asp Leu Ala His Ile Tyr Asp Gly Glu Leu
305 310 315 320

His Ile His Arg Ser Arg Arg Glu Val Gly Ala Ser Met Thr Arg Ser
325 330 335

Ile Gln Thr Leu Glu Met Glu Leu Ala Gln Ile Met Lys Gly Pro Tyr
340 345 350

Asp His Phe Met Gln Lys Glu Ile Tyr Glu Gln Pro Glu Ser Thr Phe
355 360 365

Asn Thr Met Arg Gly Arg Ile Asp Tyr Glu Asn Asn Lys Val Ile Leu
370 375 380

Gly Gly Leu Lys Ala Trp Leu Pro Val Val Arg Arg Ala Arg Arg Leu
385 390 395 400

Ile Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg
405 410 415

Ala Ile Phe Glu Glu Leu Ser Asp Ile Pro Val Ser Val Glu Leu Ala
420 425 430

Ser Asp Phe Leu Asp Arg Lys Cys Pro Val Phe Arg Asp Asp Val Cys
435 440 445

Val Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Thr Met Leu Ala Leu
450 455 460

Asn Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser
465 470 475 480

Val Gly Ser Ser Ile Ser Arg Val Thr His Cys Gly Val His Ile Asn
485 490 495

Ala Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln
500 505 510

Tyr Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asp Asp Arg Val
515 520 525

Ser Lys Ile Asp Arg Arg Ile Glu Ile Ile Gln Gly Leu Lys Leu Ile
530 535 540

Pro Gly Gln Ile Lys Gln Val Leu Lys Leu Glu Pro Arg Ile Lys Lys
545 550 555 560

Leu Cys Ala Thr Glu Leu Lys Asp Gln Lys Ser Leu Leu Leu Leu Gly
565 570 575

Arg Gly Tyr Gln Phe Ala Ala Ala Leu Glu Gly Ala Leu Lys Ile Lys
580 585 590

Glu Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys
595 600 605

His Gly Val Leu Ala Leu Val Asp Glu Asn Leu Pro Ile Ile Ala Phe
610 615 620

Gly Thr Arg Asp Ser Leu Phe Pro Lys Val Val Ser Ser Ile Glu Gln
625 630 635 640

Val Thr Ala Arg Lys Gly His Pro Ile Ile Ile Cys Asn Glu Asn Asp
645 650 655

Glu Val Trp Ala Gln Lys Ser Lys Ser Ile Asp Leu Gln Thr Leu Glu
660 665 670

Val Pro Gln Thr Val Asp Cys Leu Gln Gly Leu Ile Asn Ile Ile Pro
675 680 685

Leu Gln Leu Met Ser Tyr Trp Leu Ala Val Asn Lys Gly Ile Asp Val
690 695 700

Asp Phe Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
705 710 715

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<222> (1)..(2142)

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ggt gaa atc att gat aat tta att gaa ggt ttg caa cga tta gaa tat	96
Gly Glu Ile Ile Asp Asn Leu Ile Glu Gly Leu Gln Arg Leu Glu Tyr	
20 25 30	
aga ggt tat gat tca gca ggc att gct gtt gat ggg aaa tta act aaa	144
Arg Gly Tyr Asp Ser Ala Gly Ile Ala Val Asp Gly Lys Leu Thr Lys	
35 40 45	
gat cct tct aat ggt gat gaa gaa tat atg gat tct att att gtt aaa	192
Asp Pro Ser Asn Gly Asp Glu Glu Tyr Met Asp Ser Ile Ile Val Lys	
50 55 60	
act act ggt aaa gtt aaa gtt ttg aaa caa aaa atc att gat gat caa	240
Thr Thr Gly Lys Val Lys Val Leu Lys Gln Lys Ile Ile Asp Asp Gln	
65 70 75 80	
atc gat aga tcg gcc att ttt gat aat cat gtt ggt att gct cat act	288
Ile Asp Arg Ser Ala Ile Phe Asp Asn His Val Gly Ile Ala His Thr	
85 90 95	
aga tgg gct aca cat ggt caa cca aaa act gaa aat tgt cat cct cat	336
Arg Trp Ala Thr His Gly Gln Pro Lys Thr Glu Asn Cys His Pro His	
100 105 110	
aaa tca gat cca aag ggg gaa ttc att gtt gtt cat aat ggt att att	384
Lys Ser Asp Pro Lys Gly Glu Phe Ile Val Val His Asn Gly Ile Ile	
115 120 125	
act aat tat gct gct tta aga aaa tat ctt tta tca aaa gga cat gtt	432
Thr Asn Tyr Ala Ala Leu Arg Lys Tyr Leu Leu Ser Lys Gly His Val	
130 135 140	
ttt gaa agt gaa act gat act gaa tgt att gct aaa tta ttt aaa cat	480
Phe Glu Ser Glu Thr Asp Thr Glu Cys Ile Ala Lys Leu Phe Lys His	
145 150 155 160	
ttt tat gat ttg aat gtt aaa gct ggt gtt ttc cct gat ctt aat gaa	528
Phe Tyr Asp Leu Asn Val Lys Ala Gly Val Phe Pro Asp Leu Asn Glu	
165 170 175	
ttg act aaa caa gtt ttg cat gaa tta gaa ggt tct tat ggg tta tta	576
Leu Thr Lys Gln Val Leu His Glu Leu Glu Gly Ser Tyr Gly Leu Leu	
180 185 190	
gtt aaa tct tat cat tat cct gga gaa gtt tgt ggt act aga aaa ggt	624
Val Lys Ser Tyr His Tyr Pro Gly Glu Val Cys Gly Thr Arg Lys Gly	
195 200 205	
tct cca tta ttg gtt ggt gtt aaa act gat aag aaa tta aaa gtt gat	672
Ser Pro Leu Leu Val Gly Val Lys Thr Asp Lys Lys Leu Lys Val Asp	
210 215 220	

ttt gtt gac gtt gaa ttt gaa gct caa cag caa cat cga cca caa caa Phe Val Asp Val Glu Phe Glu Ala Gln Gln Gln His Arg Pro Gln Gln 225 230 235 240	720
cca caa atc aat cat aat ggt gcc act tca gct gct gaa ttg ggc ttt Pro Gln Ile Asn His Asn Gly Ala Thr Ser Ala Ala Glu Leu Gly Phe 245 250 255	768
atc cca gtg gct cca ggt gaa caa aat tta aga act tct caa tca aga Ile Pro Val Ala Pro Gly Glu Gln Asn Leu Arg Thr Ser Gln Ser Arg 260 265 270	816
gct ttc ctt tct gaa gat gat tta cct atg cca gtt gaa ttc ttt tta Ala Phe Leu Ser Glu Asp Asp Leu Pro Met Pro Val Glu Phe Phe Leu 275 280 285	864
tct tct gat cct gca tca gtg gtt caa cac acc aaa aaa gtt tta ttt Ser Ser Asp Pro Ala Ser Val Val Gln His Thr Lys Lys Val Leu Phe 290 295 300	912
tta gaa gat gat gat att gct cat atc tat gat ggg gaa tta cgt att Leu Glu Asp Asp Asp Ile Ala His Ile Tyr Asp Gly Glu Leu Arg Ile 305 310 315 320	960
cat aga gct tcg act aaa tct gct ggg gaa tct act gtt aga cca att His Arg Ala Ser Thr Lys Ser Ala Gly Glu Ser Thr Val Arg Pro Ile 325 330 335	1008
caa act tta gaa atg gaa ttg aat gaa att atg aaa ggc ccc tat aaa Gln Thr Leu Glu Met Glu Leu Asn Glu Ile Met Lys Gly Pro Tyr Lys 340 345 350	1056
cat ttt atg caa aaa gaa att ttc gaa caa cca gat tct gct ttt aat His Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Asp Ser Ala Phe Asn 355 360 365	1104
act atg aga ggt aga att gat ttt gaa aat tgt gtt gtt acc ctt ggt Thr Met Arg Gly Arg Ile Asp Phe Glu Asn Cys Val Val Thr Leu Gly 370 375 380	1152
gga tta aaa tca tgg tta tct aca att aga aga tgt aga aga atc att Gly Leu Lys Ser Trp Leu Ser Thr Ile Arg Arg Cys Arg Arg Ile Ile 385 390 395 400	1200
atg att gct tgt ggt act tca tat cat tca tgt tta gcc acg aga tca Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg Ser 405 410 415	1248
att ttt gaa gaa ttg aca gaa atc ccc gtt tcg gtt gaa tta gct tct Ile Phe Glu Glu Leu Thr Glu Ile Pro Val Ser Val Glu Leu Ala Ser 420 425 430	1296
gat ttc ttg gat aga aga tct cca gtt ttc aga gat gat act tgt gta Asp Phe Leu Asp Arg Arg Ser Pro Val Phe Arg Asp Asp Thr Cys Val 435 440 445	1344
ttt gtt tct caa tcg ggt gaa act gcc gac tcc att ttg gct tta caa Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Ser Ile Leu Ala Leu Gln 450 455 460	1392

tat tgt ttg gaa aga gga gct tta act gtt ggt atc gtt aac tct gtt Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser Val 465 470 475 480	1440
ggt tct tca atg tct aga caa acc cat tgt ggg gtt cat att aat gct Gly Ser Ser Met Ser Arg Gln Thr His Cys Gly Val His Ile Asn Ala 485 490 495	1488
ggg cca gaa att ggt gtt gcc tca act aaa gct tac aca tct caa tat Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln Tyr 500 505 510	1536
att gcc ttg gtg atg ttt gcc ctt tct tta tct aat gat tct att tcc Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asn Asp Ser Ile Ser 515 520 525	1584
aga aag gga aga cat gaa gaa att att aaa ggt tta caa aaa atc cct Arg Lys Gly Arg His Glu Glu Ile Ile Lys Gly Leu Gln Lys Ile Pro 530 535 540	1632
gaa caa att aaa caa gtt ttg aaa tta gaa aac aag atc aaa gat tta Glu Gln Ile Lys Gln Val Leu Lys Leu Glu Asn Lys Ile Lys Asp Leu 545 550 555 560	1680
tgt aat agt tca ttg aat gat caa aaa tct tta tta tta tta ggt aga Cys Asn Ser Ser Leu Asn Asp Gln Lys Ser Leu Leu Leu Leu Gly Arg 565 570 575	1728
ggt tat caa ttt gct act gct tta gaa ggg gct tta aaa att aaa gaa Gly Tyr Gln Phe Ala Thr Ala Leu Glu Gly Ala Leu Lys Ile Lys Glu 580 585 590	1776
att tct tat atg cat tct gaa ggg gta tta gct ggt gaa tta aaa cat Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys His 595 600 605	1824
ggt ata tta gca tta gtc gat gaa gat tta cca att att gcc ttt gcc Gly Ile Leu Ala Leu Val Asp Glu Asp Leu Pro Ile Ile Ala Phe Ala 610 615 620	1872
act aga gat tca tta ttt cct aaa gtt atg tcc gct att gaa caa gtc Thr Arg Asp Ser Leu Phe Pro Lys Val Met Ser Ala Ile Glu Gln Val 625 630 635 640	1920
act gct aga gat ggt aga cca att gtt att tgt aat gaa ggt gat gct Thr Ala Arg Asp Gly Arg Pro Ile Val Ile Cys Asn Glu Gly Asp Ala 645 650 655	1968
att att tct aat gat aaa gtt cat act act tta gaa gtt cca gaa acc Ile Ile Ser Asn Asp Lys Val His Thr Thr Leu Glu Val Pro Glu Thr 660 665 670	2016
gtt gat tgt tta caa ggg tta tta aat gtt att cca tta caa ttg att Val Asp Cys Leu Gln Gly Leu Leu Asn Val Ile Pro Leu Gln Leu Ile 675 680 685	2064
agt tat tgg ttg gct gtg aat aga ggt att gat gtt gat ttc cct cgt Ser Tyr Trp Leu Ala Val Asn Arg Gly Ile Asp Val Asp Phe Pro Arg 690 695 700	2112

aac ttg gct aaa tca gtt act gtt gag taa
 Asn Leu Ala Lys Ser Val Thr Val Glu
 705 710

2142

<210> 20
 <211> 713
 <212> PRT
 <213> Candida albicans
 <400> 20

Met Cys Gly Ile Phe Gly Tyr Val Asn Phe Leu Val Asp Lys Ser Arg
 1 5 10 15

Gly Glu Ile Ile Asp Asn Leu Ile Glu Gly Leu Gln Arg Leu Glu Tyr
 20 25 30

Arg Gly Tyr Asp Ser Ala Gly Ile Ala Val Asp Gly Lys Leu Thr Lys
 35 40 45

Asp Pro Ser Asn Gly Asp Glu Glu Tyr Met Asp Ser Ile Ile Val Lys
 50 55 60

Thr Thr Gly Lys Val Lys Val Leu Lys Gln Lys Ile Ile Asp Asp Gln
 65 70 75 80

Ile Asp Arg Ser Ala Ile Phe Asp Asn His Val Gly Ile Ala His Thr
 85 90 95

Arg Trp Ala Thr His Gly Gln Pro Lys Thr Glu Asn Cys His Pro His
 100 105 110

Lys Ser Asp Pro Lys Gly Glu Phe Ile Val Val His Asn Gly Ile Ile
 115 120 125

Thr Asn Tyr Ala Ala Leu Arg Lys Tyr Leu Leu Ser Lys Gly His Val
 130 135 140

Phe Glu Ser Glu Thr Asp Thr Glu Cys Ile Ala Lys Leu Phe Lys His
 145 150 155 160

Phe Tyr Asp Leu Asn Val Lys Ala Gly Val Phe Pro Asp Leu Asn Glu
 165 170 175

Leu Thr Lys Gln Val Leu His Glu Leu Glu Gly Ser Tyr Gly Leu Leu
 180 185 190

Val Lys Ser Tyr His Tyr Pro Gly Glu Val Cys Gly Thr Arg Lys Gly
195 200 205

Ser Pro Leu Leu Val Gly Val Lys Thr Asp Lys Lys Leu Lys Val Asp
210 215 220

Phe Val Asp Val Glu Phe Glu Ala Gln Gln Gln His Arg Pro Gln Gln
225 230 235 240

Pro Gln Ile Asn His Asn Gly Ala Thr Ser Ala Ala Glu Leu Gly Phe
245 250 255

Ile Pro Val Ala Pro Gly Glu Gln Asn Leu Arg Thr Ser Gln Ser Arg
260 265 270

Ala Phe Leu Ser Glu Asp Asp Leu Pro Met Pro Val Glu Phe Phe Leu
275 280 285

Ser Ser Asp Pro Ala Ser Val Val Gln His Thr Lys Lys Val Leu Phe
290 295 300

Leu Glu Asp Asp Asp Ile Ala His Ile Tyr Asp Gly Glu Leu Arg Ile
305 310 315 320

His Arg Ala Ser Thr Lys Ser Ala Gly Glu Ser Thr Val Arg Pro Ile
325 330 335

Gln Thr Leu Glu Met Glu Leu Asn Glu Ile Met Lys Gly Pro Tyr Lys
340 345 350

His Phe Met Gln Lys Glu Ile Phe Glu Gln Pro Asp Ser Ala Phe Asn
355 360 365

Thr Met Arg Gly Arg Ile Asp Phe Glu Asn Cys Val Val Thr Leu Gly
370 375 380

Gly Leu Lys Ser Trp Leu Ser Thr Ile Arg Arg Cys Arg Arg Ile Ile
385 390 395 400

Met Ile Ala Cys Gly Thr Ser Tyr His Ser Cys Leu Ala Thr Arg Ser
405 410 415

Ile Phe Glu Glu Leu Thr Glu Ile Pro Val Ser Val Glu Leu Ala Ser
420 425 430

Asp Phe Leu Asp Arg Arg Ser Pro Val Phe Arg Asp Asp Thr Cys Val
 435 440 445
 Phe Val Ser Gln Ser Gly Glu Thr Ala Asp Ser Ile Leu Ala Leu Gln
 450 455 460
 Tyr Cys Leu Glu Arg Gly Ala Leu Thr Val Gly Ile Val Asn Ser Val
 465 470 475 480
 Gly Ser Ser Met Ser Arg Gln Thr His Cys Gly Val His Ile Asn Ala
 485 490 495
 Gly Pro Glu Ile Gly Val Ala Ser Thr Lys Ala Tyr Thr Ser Gln Tyr
 500 505 510
 Ile Ala Leu Val Met Phe Ala Leu Ser Leu Ser Asn Asp Ser Ile Ser
 515 520 525
 Arg Lys Gly Arg His Glu Glu Ile Ile Lys Gly Leu Gln Lys Ile Pro
 530 535 540
 Glu Gln Ile Lys Gln Val Leu Lys Leu Glu Asn Lys Ile Lys Asp Leu
 545 550 555 560
 Cys Asn Ser Ser Leu Asn Asp Gln Lys Ser Leu Leu Leu Leu Gly Arg
 565 570 575
 Gly Tyr Gln Phe Ala Thr Ala Leu Glu Gly Ala Leu Lys Ile Lys Glu
 580 585 590
 Ile Ser Tyr Met His Ser Glu Gly Val Leu Ala Gly Glu Leu Lys His
 595 600 605
 Gly Ile Leu Ala Leu Val Asp Glu Asp Leu Pro Ile Ile Ala Phe Ala
 610 615 620
 Thr Arg Asp Ser Leu Phe Pro Lys Val Met Ser Ala Ile Glu Gln Val
 625 630 635 640
 Thr Ala Arg Asp Gly Arg Pro Ile Val Ile Cys Asn Glu Gly Asp Ala
 645 650 655
 Ile Ile Ser Asn Asp Lys Val His Thr Thr Leu Glu Val Pro Glu Thr
 660 665 670

Val Asp Cys Leu Gln Gly Leu Leu Asn Val Ile Pro Leu Gln Leu Ile
675 680 685

Ser Tyr Trp Leu Ala Val Asn Arg Gly Ile Asp Val Asp Phe Pro Arg
690 695 700

Asn Leu Ala Lys Ser Val Thr Val Glu
705 710

<210> 21
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 21
gatcgggtctc gcatgtgtgg aatcgtaggt tatatcggtc 40

<210> 22
<211> 43
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 22
gatcctcgag ttactccaca gtaacactct tcgcaagggtt acg 43

<210> 23
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 23
gatcgggtctc gcatgtgtgg tatctttggt tac 33

<210> 24
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 24
gatcgaattc ttattcgacg gtaacagatt tag 33

<210> 25
 <211> 36
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 25
 gatcgggtctc gcatgtgtgg tatttttggg tacgtc 36

 <210> 26
 <211> 35
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 26
 gatcctcgag ttactcaaca gtaactgatt tagcc 35

 <210> 27
 <211> 35
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 27
 gcgggtaccc atatgtgtgg tatttttggg tacgt 35

 <210> 28
 <211> 35
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 28
 gcgggatacct tactcaacag taactgattt agcca 35

 <210> 29
 <211> 480
 <212> DNA
 <213> Saccharomyces cerevisiae

 <220>
 <221> CDS
 <222> (1)..(480)
 <223>

 <400> 29

atg agc tta ccc gat gga ttt tat ata agg cga atg gaa gag ggg gat 48
 Met Ser Leu Pro Asp Gly Phe Tyr Ile Arg Arg Met Glu Glu Gly Asp
 1 5 10 15
 ttg gaa cag gtc act gag acg cta aag gtt ttg acc acc gtg ggc act 96
 Leu Glu Gln Val Thr Glu Thr Leu Lys Val Leu Thr Thr Val Gly Thr
 20 25 30
 att acc ccc gaa tcc ttc agc aaa ctc ata aaa tac tgg aat gaa gcc 144
 Ile Thr Pro Glu Ser Phe Ser Lys Leu Ile Lys Tyr Trp Asn Glu Ala
 35 40 45
 aca gta tgg aat gat aac gaa gat aaa aaa ata atg caa tat aac ccc 192
 Thr Val Trp Asn Asp Asn Glu Asp Lys Lys Ile Met Gln Tyr Asn Pro
 50 55 60
 atg gtg att gtg gac aag cgc acc gag acg gtt gcc gct acg ggg aat 240
 Met Val Ile Val Asp Lys Arg Thr Glu Thr Val Ala Ala Thr Gly Asn
 65 70 75 80
 atc atc atc gaa aga aag atc att cat gaa ctg ggg cta tgt ggc cac 288
 Ile Ile Ile Glu Arg Lys Ile Ile His Glu Leu Gly Leu Cys Gly His
 85 90 95
 atc gag gac att gca gta aac tcc aag tat cag ggc caa ggt ttg ggc 336
 Ile Glu Asp Ile Ala Val Asn Ser Lys Tyr Gln Gly Gln Gly Leu Gly
 100 105 110
 aag ctc ttg att gat caa ttg gta act atc ggc ttt gac tac ggt tgt 384
 Lys Leu Leu Ile Asp Gln Leu Val Thr Ile Gly Phe Asp Tyr Gly Cys
 115 120 125
 tat aag att att tta gat tgc gat gag aaa aat gtc aaa ttc tat gaa 432
 Tyr Lys Ile Ile Leu Asp Cys Asp Glu Lys Asn Val Lys Phe Tyr Glu
 130 135 140
 aaa tgt ggg ttt agc aac gca ggc gtg gaa atg caa att aga aaa tag 480
 Lys Cys Gly Phe Ser Asn Ala Gly Val Glu Met Gln Ile Arg Lys
 145 150 155

<210> 30
 <211> 159
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 30

Met Ser Leu Pro Asp Gly Phe Tyr Ile Arg Arg Met Glu Glu Gly Asp
 1 5 10 15

Leu Glu Gln Val Thr Glu Thr Leu Lys Val Leu Thr Thr Val Gly Thr
 20 25 30

Ile Thr Pro Glu Ser Phe Ser Lys Leu Ile Lys Tyr Trp Asn Glu Ala
 35 40 45

Thr Val Trp Asn Asp Asn Glu Asp Lys Lys Ile Met Gln Tyr Asn Pro
50 55 60

Met Val Ile Val Asp Lys Arg Thr Glu Thr Val Ala Ala Thr Gly Asn
65 70 75 80

Ile Ile Ile Glu Arg Lys Ile Ile His Glu Leu Gly Leu Cys Gly His
85 90 95

Ile Glu Asp Ile Ala Val Asn Ser Lys Tyr Gln Gly Gln Gly Leu Gly
100 105 110

Lys Leu Leu Ile Asp Gln Leu Val Thr Ile Gly Phe Asp Tyr Gly Cys
115 120 125

Tyr Lys Ile Ile Leu Asp Cys Asp Glu Lys Asn Val Lys Phe Tyr Glu
130 135 140

Lys Cys Gly Phe Ser Asn Ala Gly Val Glu Met Gln Ile Arg Lys
145 150 155

<210> 31
<211> 450
<212> DNA
<213> Candida albicans

<220>
<221> CDS
<222> (1)..(450)
<223>

<400> 31
atg atg tta cca caa ggt tat aca ttc aga aaa cta aaa ctt act gat 48
Met Met Leu Pro Gln Gly Tyr Thr Phe Arg Lys Leu Lys Leu Thr Asp
1 5 10 15
tat gat aat caa tat tta gaa act tta aaa gtt ttg acg aca gtt ggt 96
Tyr Asp Asn Gln Tyr Leu Glu Thr Leu Lys Val Leu Thr Thr Val Gly
20 25 30
gaa att tcc aaa gaa gat ttc act gaa ttg tat aat cat tgg tct tca 144
Glu Ile Ser Lys Glu Asp Phe Thr Glu Leu Tyr Asn His Trp Ser Ser
35 40 45
ttg cca tct att tat cat cca tat gta atc acc aat gca tca ggt ata 192
Leu Pro Ser Ile Tyr His Pro Tyr Val Ile Thr Asn Ala Ser Gly Ile
50 55 60
gtg gta gcc acg ggg atg tta ttt gtg gag aaa aaa ttg att cat gaa 240
Val Val Ala Thr Gly Met Leu Phe Val Glu Lys Lys Leu Ile His Glu
65 70 75 80

tgt ggt aaa gtt ggt cat att gaa gat att tca gtt gct aaa tct gaa	288
Cys Gly Lys Val Gly His Ile Glu Asp Ile Ser Val Ala Lys Ser Glu	
85 90 95	

caa ggt aaa aaa ttg gga tat tat tta gtc act tca tta acc aaa gtt	336
Gln Gly Lys Lys Leu Gly Tyr Tyr Leu Val Thr Ser Leu Thr Lys Val	
100 105 110	

gct caa gag aat gat tgt tac aaa gtc att tta gat tgt tct cct gaa	384
Ala Gln Glu Asn Asp Cys Tyr Lys Val Ile Leu Asp Cys Ser Pro Glu	
115 120 125	

aat gtt ggc ttt tat gaa aaa tgt ggt tat aaa gat ggt ggt gtt gaa	432
Asn Val Gly Phe Tyr Glu Lys Cys Gly Tyr Lys Asp Gly Gly Val Glu	
130 135 140	

atg gta tgt aga ttc tag	450
Met Val Cys Arg Phe	
145	

<210> 32
 <211> 149
 <212> PRT
 <213> Candida albicans

<400> 32

Met Met Leu Pro Gln Gly Tyr Thr Phe Arg Lys Leu Lys Leu Thr Asp
1 5 10 15

Tyr Asp Asn Gln Tyr Leu Glu Thr Leu Lys Val Leu Thr Thr Val Gly
20 25 30

Glu Ile Ser Lys Glu Asp Phe Thr Glu Leu Tyr Asn His Trp Ser Ser
35 40 45

Leu Pro Ser Ile Tyr His Pro Tyr Val Ile Thr Asn Ala Ser Gly Ile
50 55 60

Val Val Ala Thr Gly Met Leu Phe Val Glu Lys Lys Leu Ile His Glu
65 70 75 80

Cys Gly Lys Val Gly His Ile Glu Asp Ile Ser Val Ala Lys Ser Glu
85 90 95

Gln Gly Lys Lys Leu Gly Tyr Tyr Leu Val Thr Ser Leu Thr Lys Val
100 105 110

Ala Gln Glu Asn Asp Cys Tyr Lys Val Ile Leu Asp Cys Ser Pro Glu
115 120 125

Asn Val Gly Phe Tyr Glu Lys Cys Gly Tyr Lys Asp Gly Gly Val Glu
 130 135 140

Met Val Cys Arg Phe
 145

<210> 33
 <211> 450
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (1)..(450)
 <223>

<400> 33
 atg gct gag aca ttc aag atc cga aaa ctg gag atc tcc gat aag aga 48
 Met Ala Glu Thr Phe Lys Ile Arg Lys Leu Glu Ile Ser Asp Lys Arg
 1 5 10 15
 aaa gga ttc atc gag ctt cta ggt caa cta acc gtc acc gga tca gta 96
 Lys Gly Phe Ile Glu Leu Leu Gly Gln Leu Thr Val Thr Gly Ser Val
 20 25 30
 aca gac gaa gaa ttc gat cgg cga ttc gaa gaa atc aga tcg tat ggt 144
 Thr Asp Glu Glu Phe Asp Arg Arg Phe Glu Glu Ile Arg Ser Tyr Gly
 35 40 45
 gac gac cac gtg atc tgc gtg atc gaa gaa gaa act tcg gga aaa atc 192
 Asp Asp His Val Ile Cys Val Ile Glu Glu Glu Thr Ser Gly Lys Ile
 50 55 60
 gct gct acg ggt agt gtg atg ata gag aag aag ttt ctg agg aat tgc 240
 Ala Ala Thr Gly Ser Val Met Ile Glu Lys Lys Phe Leu Arg Asn Cys
 65 70 75 80
 ggt aaa gct ggg cac att gaa gac gtt gtt gtg gat tca agg ttt cgc 288
 Gly Lys Ala Gly His Ile Glu Asp Val Val Val Asp Ser Arg Phe Arg
 85 90 95
 ggg aaa cag ctg ggg aag aaa gtt gtt gag ttt ctt atg gat cat tgc 336
 Gly Lys Gln Leu Gly Lys Lys Val Val Glu Phe Leu Met Asp His Cys
 100 105 110
 aaa tca atg ggt tgc tat aag gtg att cta gat tgt agt gtg gag aac 384
 Lys Ser Met Gly Cys Tyr Lys Val Ile Leu Asp Cys Ser Val Glu Asn
 115 120 125
 aaa gtg ttc tat gag aaa tgt ggg atg agt aat aaa tcg att caa atg 432
 Lys Val Phe Tyr Glu Lys Cys Gly Met Ser Asn Lys Ser Ile Gln Met
 130 135 140
 tct aag tac ttc gat taa 450
 Ser Lys Tyr Phe Asp
 145

<210> 34
 <211> 149
 <212> PRT
 <213> Arabidopsis thaliana

<400> 34

Met Ala Glu Thr Phe Lys Ile Arg Lys Leu Glu Ile Ser Asp Lys Arg
 1 5 10 15

Lys Gly Phe Ile Glu Leu Leu Gly Gln Leu Thr Val Thr Gly Ser Val
 20 25 30

Thr Asp Glu Glu Phe Asp Arg Arg Phe Glu Glu Ile Arg Ser Tyr Gly
 35 40 45

Asp Asp His Val Ile Cys Val Ile Glu Glu Glu Thr Ser Gly Lys Ile
 50 55 60

Ala Ala Thr Gly Ser Val Met Ile Glu Lys Lys Phe Leu Arg Asn Cys
 65 70 75 80

Gly Lys Ala Gly His Ile Glu Asp Val Val Val Asp Ser Arg Phe Arg
 85 90 95

Gly Lys Gln Leu Gly Lys Lys Val Val Glu Phe Leu Met Asp His Cys
 100 105 110

Lys Ser Met Gly Cys Tyr Lys Val Ile Leu Asp Cys Ser Val Glu Asn
 115 120 125

Lys Val Phe Tyr Glu Lys Cys Gly Met Ser Asn Lys Ser Ile Gln Met
 130 135 140

Ser Lys Tyr Phe Asp
 145

<210> 35
 <211> 43
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 35
 gatcgggtctc gcatgagctt acccgatgga ttttatataa ggc

43

<210> 36
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 36
gatcctcgag ctattttcta atttgcattt ccacgcctgc

40

<210> 37
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 37
gatcggtctc gcatgatgtt accacaaggt tatac

35

<210> 38
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 38
gatcctcgag ctagaatcta cataccattt caac

34

<210> 39
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 39
gatggtctcg catggctgag acattcaaga tc

32

<210> 40
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 40
gatcctcgag ttaatcgaag tacttagaca tttgaatc

38

<210> 41
 <211> 801
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(801)
 <223>

<400> 41
 atg aga ctg atc ccc ctg act acc gct gaa cag gtc ggc aaa tgg gct 48
 Met Arg Leu Ile Pro Leu Thr Thr Ala Glu Gln Val Gly Lys Trp Ala
 1 5 10 15
 gct cgc cat atc gtc aat cgt atc aat gcg ttc aaa ccg act gcc gat 96
 Ala Arg His Ile Val Asn Arg Ile Asn Ala Phe Lys Pro Thr Ala Asp
 20 25 30
 cgt ccg ttt gta ctg ggc ctg ccg act ggc ggc acg ccg atg acc acc 144
 Arg Pro Phe Val Leu Gly Leu Pro Thr Gly Gly Thr Pro Met Thr Thr
 35 40 45
 tat aaa gcg tta gtc gaa atg cat aaa gca ggc cag gtc agc ttt aag 192
 Tyr Lys Ala Leu Val Glu Met His Lys Ala Gly Gln Val Ser Phe Lys
 50 55 60
 cac gtt gtc acc ttc aac atg gac gaa tat gtc ggt ctg ccg aaa gag 240
 His Val Val Thr Phe Asn Met Asp Glu Tyr Val Gly Leu Pro Lys Glu
 65 70 75 80
 cat ccg gaa agc tac tac agc ttt atg cac cgt aat ttc ttc gat cac 288
 His Pro Glu Ser Tyr Tyr Ser Phe Met His Arg Asn Phe Phe Asp His
 85 90 95
 gtt gat att cca gca gaa aac atc aac ctt ctc aac ggc aac gcc ccg 336
 Val Asp Ile Pro Ala Glu Asn Ile Asn Leu Leu Asn Gly Asn Ala Pro
 100 105 110
 gat atc gac gcc gag tgc cgc cag tat gaa gaa aaa atc cgt tct tac 384
 Asp Ile Asp Ala Glu Cys Arg Gln Tyr Glu Glu Lys Ile Arg Ser Tyr
 115 120 125
 gga aaa att cat ctg ttt atg ggc ggt gta ggt aac gac ggt cat att 432
 Gly Lys Ile His Leu Phe Met Gly Gly Val Gly Asn Asp Gly His Ile
 130 135 140
 gca ttt aac gaa ccg gcg tct tct ctg gct tct cgt act cgt atc aaa 480
 Ala Phe Asn Glu Pro Ala Ser Ser Leu Ala Ser Arg Thr Arg Ile Lys
 145 150 155 160
 acc ctg act cat gac act cgc gtc gca aac tct cgt ttc ttt gat aac 528
 Thr Leu Thr His Asp Thr Arg Val Ala Asn Ser Arg Phe Phe Asp Asn
 165 170 175
 gat gtt aat cag gtg cca aaa tat gcc ctg act gtc ggt gtt ggt aca 576
 Asp Val Asn Gln Val Pro Lys Tyr Ala Leu Thr Val Gly Val Gly Thr
 180 185 190

ctg ctg gat gcc gaa gaa gtg atg att ctg gtg ctg ggt agc cag aaa	624
Leu Leu Asp Ala Glu Glu Val Met Ile Leu Val Leu Gly Ser Gln Lys	
195 200 205	
gca ctg gcg ctg cag gcc gcc gtt gaa ggt tgc gtg aac cat atg tgg	672
Ala Leu Ala Leu Gln Ala Ala Val Glu Gly Cys Val Asn His Met Trp	
210 215 220	
acc atc agc tgt ctg caa ctg cat ccg aaa gcg atc atg gtg tgc gat	720
Thr Ile Ser Cys Leu Gln Leu His Pro Lys Ala Ile Met Val Cys Asp	
225 230 235 240	
gaa cct tcc acc atg gag ctg aaa gtt aag act tta aga tat ttc aat	768
Glu Pro Ser Thr Met Glu Leu Lys Val Lys Thr Leu Arg Tyr Phe Asn	
245 250 255	
gaa tta gaa gca gaa aat atc aaa ggt ctg taa	801
Glu Leu Glu Ala Glu Asn Ile Lys Gly Leu	
260 265	

<210> 42
 <211> 266
 <212> PRT
 <213> Escherichia coli

<400> 42

Met Arg Leu Ile Pro Leu Thr Thr Ala Glu Gln Val Gly Lys Trp Ala	
1 5 10 15	
Ala Arg His Ile Val Asn Arg Ile Asn Ala Phe Lys Pro Thr Ala Asp	
20 25 30	
Arg Pro Phe Val Leu Gly Leu Pro Thr Gly Gly Thr Pro Met Thr Thr	
35 40 45	
Tyr Lys Ala Leu Val Glu Met His Lys Ala Gly Gln Val Ser Phe Lys	
50 55 60	
His Val Val Thr Phe Asn Met Asp Glu Tyr Val Gly Leu Pro Lys Glu	
65 70 75 80	
His Pro Glu Ser Tyr Tyr Ser Phe Met His Arg Asn Phe Phe Asp His	
85 90 95	
Val Asp Ile Pro Ala Glu Asn Ile Asn Leu Leu Asn Gly Asn Ala Pro	
100 105 110	
Asp Ile Asp Ala Glu Cys Arg Gln Tyr Glu Glu Lys Ile Arg Ser Tyr	
115 120 125	

Gly Lys Ile His Leu Phe Met Gly Gly Val Gly Asn Asp Gly His Ile
 130 135 140

Ala Phe Asn Glu Pro Ala Ser Ser Leu Ala Ser Arg Thr Arg Ile Lys
 145 150 155 160

Thr Leu-Thr His Asp Thr Arg Val Ala Asn Ser Arg Phe Phe Asp Asn
 165 170 175

Asp Val Asn Gln Val Pro Lys Tyr Ala Leu Thr Val Gly Val Gly Thr
 180 185 190

Leu Leu Asp Ala Glu Glu Val Met Ile Leu Val Leu Gly Ser Gln Lys
 195 200 205

Ala Leu Ala Leu Gln Ala Ala Val Glu Gly Cys Val Asn His Met Trp
 210 215 220

Thr Ile Ser Cys Leu Gln Leu His Pro Lys Ala Ile Met Val Cys Asp
 225 230 235 240

Glu Pro Ser Thr Met Glu Leu Lys Val Lys Thr Leu Arg Tyr Phe Asn
 245 250 255

Glu Leu Glu Ala Glu Asn Ile Lys Gly Leu
 260 265

<210> 43
 <211> 31
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 43
 gatggtctcg catgagactg atccccctga c

31

<210> 44
 <211> 43
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 44
 gatcctcgag ttacagacct ttgatatttt ctgcttctaa ttc

43

<210> 45
 <211> 43
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 45
 gatcctcgag ttacagacct ttgatatttt ctgcttctaa ttc 43

 <210> 46
 <211> 32
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 46
 gatcctgcag tcatgctgct aataatctat cc 32

 <210> 47
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 47
 gatctacgta agcaaccgca cctgtggc 28

 <210> 48
 <211> 36
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 48
 gatccaattg atccggatat agttctctct ttcagc 36

 <210> 49
 <211> 41
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 49
 gatgcggcgg catgttgaat aatgctatga gcgtagtgat c 41

<210> 50
 <211> 37
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 50
 gatcgtcgac ttagtacagc ggcttaccgc tactgtc 37

<210> 51
 <211> 35
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 51
 gatgcggccg catggcaatg acttaccacc tggac 35

<210> 52
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 52
 cgtaccagc tgctctgcct gaagcaccc 29

<210> 53
 <211> 1338
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)..(1338)
 <223>

 <400> 53
 atg agt aat cgt aaa tat ttc ggt acc gat ggg att cgt ggt cgt gta 48
 Met Ser Asn Arg Lys Tyr Phe Gly Thr Asp Gly Ile Arg Gly Arg Val
 1 5 10 15

ggg gat gcg ccg atc aca cct gat ttt gtg ctt aag ctg ggt tgg gcc 96
 Gly Asp Ala Pro Ile Thr Pro Asp Phe Val Leu Lys Leu Gly Trp Ala
 20 25 30

gcg ggt aaa gtg ctg gcg cgc cac ggc tcc cgt aag att att att ggt 144
 Ala Gly Lys Val Leu Ala Arg His Gly Ser Arg Lys Ile Ile Ile Gly
 35 40 45

aaa gac acg cgt att tct ggc tat atg ctg gag tca gca ctg gaa gcg Lys Asp Thr Arg Ile Ser Gly Tyr Met Leu Glu Ser Ala Leu Glu Ala 50 55 60	192
ggc ctg gcg gca gcg ggc ctt tcc gca ctc ttc act ggc ccg atg cca Gly Leu Ala Ala Ala Gly Leu Ser Ala Leu Phe Thr Gly Pro Met Pro 65 70 75 80	240
aca ccg gcc gtg gct tat ctg acg cgt acc ttc cgc gca gag gcc gga Thr Pro Ala Val Ala Tyr Leu Thr Arg Thr Phe Arg Ala Glu Ala Gly 85 90 95	288
att gtg ata tct gca tct cat aac ccg ttc tac gat aat ggc att aaa Ile Val Ile Ser Ala Ser His Asn Pro Phe Tyr Asp Asn Gly Ile Lys 100 105 110	336
ttc ttc tct atc gac ggc acc aaa ctg ccg gat gcg gta gaa gag gcc Phe Phe Ser Ile Asp Gly Thr Lys Leu Pro Asp Ala Val Glu Glu Ala 115 120 125	384
atc gaa gcg gaa atg gaa aag gag atc agc tgc gtt gat tct gca gaa Ile Glu Ala Glu Met Glu Lys Glu Ile Ser Cys Val Asp Ser Ala Glu 130 135 140	432
ctg ggt aaa gcc agc cgt atc gtt gat gcc gcg ggt cgc tat atc gag Leu Gly Lys Ala Ser Arg Ile Val Asp Ala Ala Gly Arg Tyr Ile Glu 145 150 155 160	480
ttt tgc aaa gcc acg ttc ccg aac gaa ctt agc ctc agt gaa ctg aag Phe Cys Lys Ala Thr Phe Pro Asn Glu Leu Ser Leu Ser Glu Leu Lys 165 170 175	528
att gtg gtg gat tgt gca aac ggt gcg act tat cac atc gcg ccg aac Ile Val Val Asp Cys Ala Asn Gly Ala Thr Tyr His Ile Ala Pro Asn 180 185 190	576
gtg ctg cgc gaa ctg ggg gcg aac gtt atc gct atc ggt tgt gag cca Val Leu Arg Glu Leu Gly Ala Asn Val Ile Ala Ile Gly Cys Glu Pro 195 200 205	624
aac ggt gta aac atc aat gcc gaa gtg ggg gct acc gac gtt cgc gcg Asn Gly Val Asn Ile Asn Ala Glu Val Gly Ala Thr Asp Val Arg Ala 210 215 220	672
ctc cag gct cgt gtg ctg gct gaa aaa gcg gat ctc ggt att gcc ttc Leu Gln Ala Arg Val Leu Ala Glu Lys Ala Asp Leu Gly Ile Ala Phe 225 230 235 240	720
gac ggc gat ggc gat cgc gtg att atg gtt gac cat gaa ggc aat aaa Asp Gly Asp Gly Asp Arg Val Ile Met Val Asp His Glu Gly Asn Lys 245 250 255	768
gtc gat ggc gat cag atc atg tat atc atc gcg cgt gaa ggt ctt cgt Val Asp Gly Asp Gln Ile Met Tyr Ile Ile Ala Arg Glu Gly Leu Arg 260 265 270	816
cag ggc cag ctg cgt ggt ggc gct gtg ggt aca ttg atg agc aac atg Gln Gly Gln Leu Arg Gly Gly Ala Val Gly Thr Leu Met Ser Asn Met 275 280 285	864

ggg ctt gaa ctg gcg ctg aaa cag tta gga att cca ttt gcg cgc gcg	912
Gly Leu Glu Leu Ala Leu Lys Gln Leu Gly Ile Pro Phe Ala Arg Ala	
290 295 300	
aaa gtg ggt gac cgc tac gta ctg gaa aaa atg cag gag aaa ggc tgg	960
Lys Val Gly Asp Arg Tyr Val Leu Glu Lys Met Gln Glu Lys Gly Trp	
305 310 315 320	
cgt atc ggt gca gag aat tcc ggt cat gtg atc ctg ctg gat aaa act	1008
Arg Ile Gly Ala Glu Asn Ser Gly His Val Ile Leu Leu Asp Lys Thr	
325 330 335	
act acc ggt gac ggc atc gtt gct ggc ttg cag gtg ctg gcg gcg atg	1056
Thr Thr Gly Asp Gly Ile Val Ala Gly Leu Gln Val Leu Ala Ala Met	
340 345 350	
gca cgt aac cat atg agc ctg cac gac ctt tgc agc ggc atg aaa atg	1104
Ala Arg Asn His Met Ser Leu His Asp Leu Cys Ser Gly Met Lys Met	
355 360 365	
ttc ccg cag att ctg gtt aac gta cgt tac acc gca ggt agc ggc gat	1152
Phe Pro Gln Ile Leu Val Asn Val Arg Tyr Thr Ala Gly Ser Gly Asp	
370 375 380	
cca ctt gag cat gag tca gtt aaa gcc gtg acc gca gag gtt gaa gct	1200
Pro Leu Glu His Glu Ser Val Lys Ala Val Thr Ala Glu Val Glu Ala	
385 390 395 400	
gcg ctg ggc aac cgt gga cgc gtg ttg ctg cgt aaa tcc ggc acc gaa	1248
Ala Leu Gly Asn Arg Gly Arg Val Leu Leu Arg Lys Ser Gly Thr Glu	
405 410 415	
ccg tta att cgc gtg atg gtg gaa ggc gaa gac gaa gcg cag gtg act	1296
Pro Leu Ile Arg Val Met Val Glu Gly Glu Asp Glu Ala Gln Val Thr	
420 425 430	
gaa ttt gca cac cgc atc gcc gat gca gta aaa gcc gtt taa	1338
Glu Phe Ala His Arg Ile Ala Asp Ala Val Lys Ala Val	
435 440 445	

<210> 54
 <211> 445
 <212> PRT
 <213> Escherichia coli

<400> 54

Met Ser Asn Arg Lys Tyr Phe Gly Thr Asp Gly Ile Arg Gly Arg Val
1 5 10 15

Gly Asp Ala Pro Ile Thr Pro Asp Phe Val Leu Lys Leu Gly Trp Ala
20 25 30

Ala Gly Lys Val Leu Ala Arg His Gly Ser Arg Lys Ile Ile Ile Gly
35 40 45

Lys Asp Thr Arg Ile Ser Gly Tyr Met Leu Glu Ser Ala Leu Glu Ala
 50 55 60

Gly Leu Ala Ala Ala Gly Leu Ser Ala Leu Phe Thr Gly Pro Met Pro
 65 70 75 80

Thr Pro Ala Val Ala Tyr Leu Thr Arg Thr Phe Arg Ala Glu Ala Gly
 85 90 95

Ile Val Ile Ser Ala Ser His Asn Pro Phe Tyr Asp Asn Gly Ile Lys
 100 105 110

Phe Phe Ser Ile Asp Gly Thr Lys Leu Pro Asp Ala Val Glu Glu Ala
 115 120 125

Ile Glu Ala Glu Met Glu Lys Glu Ile Ser Cys Val Asp Ser Ala Glu
 130 135 140

Leu Gly Lys Ala Ser Arg Ile Val Asp Ala Ala Gly Arg Tyr Ile Glu
 145 150 155 160

Phe Cys Lys Ala Thr Phe Pro Asn Glu Leu Ser Leu Ser Glu Leu Lys
 165 170 175

Ile Val Val Asp Cys Ala Asn Gly Ala Thr Tyr His Ile Ala Pro Asn
 180 185 190

Val Leu Arg Glu Leu Gly Ala Asn Val Ile Ala Ile Gly Cys Glu Pro
 195 200 205

Asn Gly Val Asn Ile Asn Ala Glu Val Gly Ala Thr Asp Val Arg Ala
 210 215 220

Leu Gln Ala Arg Val Leu Ala Glu Lys Ala Asp Leu Gly Ile Ala Phe
 225 230 235 240

Asp Gly Asp Gly Asp Arg Val Ile Met Val Asp His Glu Gly Asn Lys
 245 250 255

Val Asp Gly Asp Gln Ile Met Tyr Ile Ile Ala Arg Glu Gly Leu Arg
 260 265 270

Gln Gly Gln Leu Arg Gly Gly Ala Val Gly Thr Leu Met Ser Asn Met
 275 280 285

Gly Leu Glu Leu Ala Leu Lys Gln Leu Gly Ile Pro Phe Ala Arg Ala
 290 295 300

Lys Val Gly Asp Arg Tyr Val Leu Glu Lys Met Gln Glu Lys Gly Trp
 305 310 315 320

Arg Ile Gly Ala Glu Asn Ser Gly His Val Ile Leu Leu Asp Lys Thr
 325 330 335

Thr Thr Gly Asp Gly Ile Val Ala Gly Leu Gln Val Leu Ala Ala Met
 340 345 350

Ala Arg Asn His Met Ser Leu His Asp Leu Cys Ser Gly Met Lys Met
 355 360 365

Phe Pro Gln Ile Leu Val Asn Val Arg Tyr Thr Ala Gly Ser Gly Asp
 370 375 380

Pro Leu Glu His Glu Ser Val Lys Ala Val Thr Ala Glu Val Glu Ala
 385 390 395 400

Ala Leu Gly Asn Arg Gly Arg Val Leu Leu Arg Lys Ser Gly Thr Glu
 405 410 415

Pro Leu Ile Arg Val Met Val Glu Gly Glu Asp Glu Ala Gln Val Thr
 420 425 430

Glu Phe Ala His Arg Ile Ala Asp Ala Val Lys Ala Val
 435 440 445

<210> 55
 <211> 1371
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1371)
 <223>

<400> 55
 atg ttg aat aat gct atg agc gta gtg atc ctt gcc gca ggc aaa ggc 48
 Met Leu Asn Asn Ala Met Ser Val Val Ile Leu Ala Ala Gly Lys Gly
 1 5 10 15
 acg cgc atg tat tcc gat ctt ccg aaa gtg ctg cat acc ctt gcc ggc 96
 Thr Arg Met Tyr Ser Asp Leu Pro Lys Val Leu His Thr Leu Ala Gly
 20 25 30

aaa gcg atg gtt cag cat gtc att gat gct gcg aat gaa tta ggc gca Lys Ala Met Val Gln His Val Ile Asp Ala Ala Asn Glu Leu Gly Ala 35 40 45	144
gcg cac gtt cac ctg gtg tac ggt cac ggc ggc gat ctg cta aaa cag Ala His Val His Leu Val Tyr Gly His Gly Gly Asp Leu Leu Lys Gln 50 55 60	192
gcg ctg aaa gac gac aac ctt aac tgg gtg ctt cag gca gag cag ctg Ala Leu Lys Asp Asp Asn Leu Asn Trp Val Leu Gln Ala Glu Gln Leu 65 70 75 80	240
ggg acg ggt cat gca atg cag cag gcc gca cct ttc ttt gcc gat gat Gly Thr Gly His Ala Met Gln Gln Ala Ala Pro Phe Phe Ala Asp Asp 85 90 95	288
gaa gac att tta atg ctc tac ggc gac gtg ccg ctg atc tct gtc gaa Glu Asp Ile Leu Met Leu Tyr Gly Asp Val Pro Leu Ile Ser Val Glu 100 105 110	336
aca ctc cag cgt ctg cgt gat gct aaa ccg cag ggt ggc att ggt ctg Thr Leu Gln Arg Leu Arg Asp Ala Lys Pro Gln Gly Gly Ile Gly Leu 115 120 125	384
ctg acg gtg aaa ctg gat gat ccg acc ggt tat gga cgt atc acc cgt Leu Thr Val Lys Leu Asp Asp Pro Thr Gly Tyr Gly Arg Ile Thr Arg 130 135 140	432
gaa aac ggc aaa gtt acc ggc att gtt gag cac aaa gat gcc acc gac Glu Asn Gly Lys Val Thr Gly Ile Val Glu His Lys Asp Ala Thr Asp 145 150 155 160	480
gag cag cgt cag att cag gag atc aac acc ggc att ctg att gcc aac Glu Gln Arg Gln Ile Gln Glu Ile Asn Thr Gly Ile Leu Ile Ala Asn 165 170 175	528
ggc gca gat atg aaa cgc tgg ctg gcg aag ctg acc aac aat aat gct Gly Ala Asp Met Lys Arg Trp Leu Ala Lys Leu Thr Asn Asn Asn Ala 180 185 190	576
cag ggc gaa tac tac atc acc gac att att gcg ctg gcg tat cag gaa Gln Gly Glu Tyr Tyr Ile Thr Asp Ile Ile Ala Leu Ala Tyr Gln Glu 195 200 205	624
ggg cgt gaa atc gtc gcc gtt cat ccg caa cgt tta agc gaa gta gaa Gly Arg Glu Ile Val Ala Val His Pro Gln Arg Leu Ser Glu Val Glu 210 215 220	672
ggc gtg aat aac cgc ctg caa ctc tcc cgt ctg gag cgt gtt tat cag Gly Val Asn Asn Arg Leu Gln Leu Ser Arg Leu Glu Arg Val Tyr Gln 225 230 235 240	720
tcc gaa cag gct gaa aaa ctg ctg tta gca ggc gtt atg ctg cgc gat Ser Glu Gln Ala Glu Lys Leu Leu Leu Ala Gly Val Met Leu Arg Asp 245 250 255	768
cca gcg cgt ttt gat ctg cgt ggt acg cta act cac ggc cgc gat gtt Pro Ala Arg Phe Asp Leu Arg Gly Thr Leu Thr His Gly Arg Asp Val 260 265 270	816

gaa att gat act aac gtt atc atc gag ggc aac gtg act ctc ggt cat	864
Glu Ile Asp Thr Asn Val Ile Ile Glu Gly Asn Val Thr Leu Gly His	
275 280 285	
cgc gtg aaa att ggc acc ggt tgc gtg att aaa aac agc gtg att ggc	912
Arg Val Lys Ile Gly Thr Gly Cys Val Ile Lys Asn Ser Val Ile Gly	
290 295 300	
gat gat tgc gaa atc agt ccg tat acc gtt gtg gaa gat gcg aat ctg	960
Asp Asp Cys Glu Ile Ser Pro Tyr Thr Val Val Glu Asp Ala Asn Leu	
305 310 315 320	
gca gcg gcc tgt acc att ggc ccg ttt gcc cgt ttg cgt cct ggt gct	1008
Ala Ala Ala Cys Thr Ile Gly Pro Phe Ala Arg Leu Arg Pro Gly Ala	
325 330 335	
gag ttg ctg gaa ggt gct cac gtc ggt aac ttc gtt gag atg aaa aaa	1056
Glu Leu Leu Glu Gly Ala His Val Gly Asn Phe Val Glu Met Lys Lys	
340 345 350	
gcg cgt ctg ggt aaa ggc tcg aaa gct ggt cat ctg act tac ctg ggc	1104
Ala Arg Leu Gly Lys Gly Ser Lys Ala Gly His Leu Thr Tyr Leu Gly	
355 360 365	
gat gcg gaa att ggc gat aac gtt aac atc ggc gcg gga acc att acc	1152
Asp Ala Glu Ile Gly Asp Asn Val Asn Ile Gly Ala Gly Thr Ile Thr	
370 375 380	
tgc aac tac gat ggt gcg aat aaa ttt aag acc att atc ggc gac gat	1200
Cys Asn Tyr Asp Gly Ala Asn Lys Phe Lys Thr Ile Ile Gly Asp Asp	
385 390 395 400	
gtg ttt gtt ggt tcc gac act cag ctg gtg gcc ccg gta aca gta ggc	1248
Val Phe Val Gly Ser Asp Thr Gln Leu Val Ala Pro Val Thr Val Gly	
405 410 415	
aaa ggc gcg acc att gct gcg ggt aca act gtg acg cgt aat gtc ggc	1296
Lys Gly Ala Thr Ile Ala Ala Gly Thr Thr Val Thr Arg Asn Val Gly	
420 425 430	
gaa aat gca tta gct atc agc cgt gtg ccg cag act cag aaa gaa ggc	1344
Glu Asn Ala Leu Ala Ile Ser Arg Val Pro Gln Thr Gln Lys Glu Gly	
435 440 445	
tgg cgt cgt ccg gta aag aaa aag tga	1371
Trp Arg Arg Pro Val Lys Lys Lys	
450 455	

<210> 56
 <211> 456
 <212> PRT
 <213> Escherichia coli

<400> 56

Met Leu Asn Asn Ala Met Ser Val Val Ile Leu Ala Ala Gly Lys Gly
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Thr Arg Met Tyr Ser Asp Leu Pro Lys Val Leu His Thr Leu Ala Gly
 20 25 30
 Lys Ala Met Val Gln His Val Ile Asp Ala Ala Asn Glu Leu Gly Ala
 35 40 45
 Ala His Val His Leu Val Tyr Gly His Gly Gly Asp Leu Leu Lys Gln
 50 55 60
 Ala Leu Lys Asp Asp Asn Leu Asn Trp Val Leu Gln Ala Glu Gln Leu
 65 70 75 80
 Gly Thr Gly His Ala Met Gln Gln Ala Ala Pro Phe Phe Ala Asp Asp
 85 90 95
 Glu Asp Ile Leu Met Leu Tyr Gly Asp Val Pro Leu Ile Ser Val Glu
 100 105 110
 Thr Leu Gln Arg Leu Arg Asp Ala Lys Pro Gln Gly Gly Ile Gly Leu
 115 120 125
 Leu Thr Val Lys Leu Asp Asp Pro Thr Gly Tyr Gly Arg Ile Thr Arg
 130 135 140
 Glu Asn Gly Lys Val Thr Gly Ile Val Glu His Lys Asp Ala Thr Asp
 145 150 155 160
 Glu Gln Arg Gln Ile Gln Glu Ile Asn Thr Gly Ile Leu Ile Ala Asn
 165 170 175
 Gly Ala Asp Met Lys Arg Trp Leu Ala Lys Leu Thr Asn Asn Asn Ala
 180 185 190
 Gln Gly Glu Tyr Tyr Ile Thr Asp Ile Ile Ala Leu Ala Tyr Gln Glu
 195 200 205
 Gly Arg Glu Ile Val Ala Val His Pro Gln Arg Leu Ser Glu Val Glu
 210 215 220
 Gly Val Asn Asn Arg Leu Gln Leu Ser Arg Leu Glu Arg Val Tyr Gln
 225 230 235 240
 Ser Glu Gln Ala Glu Lys Leu Leu Leu Ala Gly Val Met Leu Arg Asp
 245 250 255

Pro Ala Arg Phe Asp Leu Arg Gly Thr Leu Thr His Gly Arg Asp Val
 260 265 270
 Glu Ile Asp Thr Asn Val Ile Ile Glu Gly Asn Val Thr Leu Gly His
 275 280 285
 Arg Val Lys Ile Gly Thr Gly Cys Val Ile Lys Asn Ser Val Ile Gly
 290 295 300
 Asp Asp Cys Glu Ile Ser Pro Tyr Thr Val Val Glu Asp Ala Asn Leu
 305 310 315 320
 Ala Ala Ala Cys Thr Ile Gly Pro Phe Ala Arg Leu Arg Pro Gly Ala
 325 330 335
 Glu Leu Leu Glu Gly Ala His Val Gly Asn Phe Val Glu Met Lys Lys
 340 345 350
 Ala Arg Leu Gly Lys Gly Ser Lys Ala Gly His Leu Thr Tyr Leu Gly
 355 360 365
 Asp Ala Glu Ile Gly Asp Asn Val Asn Ile Gly Ala Gly Thr Ile Thr
 370 375 380
 Cys Asn Tyr Asp Gly Ala Asn Lys Phe Lys Thr Ile Ile Gly Asp Asp
 385 390 395 400
 Val Phe Val Gly Ser Asp Thr Gln Leu Val Ala Pro Val Thr Val Gly
 405 410 415
 Lys Gly Ala Thr Ile Ala Ala Gly Thr Thr Val Thr Arg Asn Val Gly
 420 425 430
 Glu Asn Ala Leu Ala Ile Ser Arg Val Pro Gln Thr Gln Lys Glu Gly
 435 440 445
 Trp Arg Arg Pro Val Lys Lys Lys
 450 455

<210> 57
 <211> 1143
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS

<222> (1) .. (1143)

<223>

<400> 57

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1 5 10 15	
ttt gcc gat gat gaa gac att tta atg ctc tac ggc gac gtg ccg ctg	96
Phe Ala Asp Asp Glu Asp Ile Leu Met Leu Tyr Gly Asp Val Pro Leu	
20 25 30	
atc tct gtc gaa aca ctc cag cgt ctg cgt gat gct aaa ccg cag ggt	144
Ile Ser Val Glu Thr Leu Gln Arg Leu Arg Asp Ala Lys Pro Gln Gly	
35 40 45	
ggc att ggt ctg ctg acg gtg aaa ctg gat gat ccg acc ggt tat gga	192
Gly Ile Gly Leu Leu Thr Val Lys Leu Asp Asp Pro Thr Gly Tyr Gly	
50 55 60	
cgt atc acc cgt gaa aac ggc aaa gtt acc ggc att gtt gag cac aaa	240
Arg Ile Thr Arg Glu Asn Gly Lys Val Thr Gly Ile Val Glu His Lys	
65 70 75 80	
gat gcc acc gac gag cag cgt cag att cag gag atc aac acc ggc att	288
Asp Ala Thr Asp Glu Gln Arg Gln Ile Gln Glu Ile Asn Thr Gly Ile	
85 90 95	
ctg att gcc aac ggc gca gat atg aaa cgc tgg ctg gcg aag ctg acc	336
Leu Ile Ala Asn Gly Ala Asp Met Lys Arg Trp Leu Ala Lys Leu Thr	
100 105 110	
aac aat aat gct cag ggc gaa tac tac atc acc gac att att gcg ctg	384
Asn Asn Asn Ala Gln Gly Glu Tyr Tyr Ile Thr Asp Ile Ile Ala Leu	
115 120 125	
gcg tat cag gaa ggg cgt gaa atc gtc gcc gtt cat ccg caa cgt tta	432
Ala Tyr Gln Glu Gly Arg Glu Ile Val Ala Val His Pro Gln Arg Leu	
130 135 140	
agc gaa gta gaa ggc gtg aat aac cgc ctg caa ctc tcc cgt ctg gag	480
Ser Glu Val Glu Gly Val Asn Asn Arg Leu Gln Leu Ser Arg Leu Glu	
145 150 155 160	
cgt gtt tat cag tcc gaa cag gct gaa aaa ctg ctg tta gca ggc gtt	528
Arg Val Tyr Gln Ser Glu Gln Ala Glu Lys Leu Leu Leu Ala Gly Val	
165 170 175	
atg ctg cgc gat cca gcg cgt ttt gat ctg cgt ggt acg cta act cac	576
Met Leu Arg Asp Pro Ala Arg Phe Asp Leu Arg Gly Thr Leu Thr His	
180 185 190	
ggg cgc gat gtt gaa att gat act aac gtt atc atc gag ggc aac gtg	624
Gly Arg Asp Val Glu Ile Asp Thr Asn Val Ile Ile Glu Gly Asn Val	
195 200 205	
act ctc ggt cat cgc gtg aaa att ggc acc ggt tgc gtg att aaa aac	672
Thr Leu Gly His Arg Val Lys Ile Gly Thr Gly Cys Val Ile Lys Asn	
210 215 220	

agc gtg att ggc gat gat tgc gaa atc agt ccg tat acc gtt gtg gaa 720
 Ser Val Ile Gly Asp Asp Cys Glu Ile Ser Pro Tyr Thr Val Val Glu
 225 230 235 240

gat gcg aat ctg gca gcg gcc tgt acc att ggc ccg ttt gcc cgt ttg 768
 Asp Ala Asn Leu Ala Ala Ala Cys Thr Ile Gly Pro Phe Ala Arg Leu
 245 250 255

cgt cct ggt gct gag ttg ctg gaa ggt gct cac gtc ggt aac ttc gtt 816
 Arg Pro Gly Ala Glu Leu Leu Glu Gly Ala His Val Gly Asn Phe Val
 260 265 270

gag atg aaa aaa gcg cgt ctg ggt aaa ggc tcg aaa gct ggt cat ctg 864
 Glu Met Lys Lys Ala Arg Leu Gly Lys Gly Ser Lys Ala Gly His Leu
 275 280 285

act tac ctg ggc gat gcg gaa att ggc gat aac gtt aac atc ggc gcg 912
 Thr Tyr Leu Gly Asp Ala Glu Ile Gly Asp Asn Val Asn Ile Gly Ala
 290 295 300

gga acc att acc tgc aac tac gat ggt gcg aat aaa ttt aag acc att 960
 Gly Thr Ile Thr Cys Asn Tyr Asp Gly Ala Asn Lys Phe Lys Thr Ile
 305 310 315 320

atc ggc gac gat gtg ttt gtt ggt tcc gac act cag ctg gtg gcc ccg 1008
 Ile Gly Asp Asp Val Phe Val Gly Ser Asp Thr Gln Leu Val Ala Pro
 325 330 335

gta aca gta ggc aaa ggc gcg acc att gct gcg ggt aca act gtg acg 1056
 Val Thr Val Gly Lys Gly Ala Thr Ile Ala Ala Gly Thr Thr Val Thr
 340 345 350

cgt aat gtc ggc gaa aat gca tta gct atc agc cgt gtg ccg cag act 1104
 Arg Asn Val Gly Glu Asn Ala Leu Ala Ile Ser Arg Val Pro Gln Thr
 355 360 365

cag aaa gaa ggc tgg cgt cgt ccg gta aag aaa aag tga 1143
 Gln Lys Glu Gly Trp Arg Arg Pro Val Lys Lys Lys
 370 375 380

<210> 58

<211> 380

<212> PRT

<213> Escherichia coli

<400> 58

Met Glu Gln Leu Gly Thr Gly His Ala Met Gln Gln Ala Ala Pro Phe
 1 5 10 15

Phe Ala Asp Asp Glu Asp Ile Leu Met Leu Tyr Gly Asp Val Pro Leu
 20 25 30

Ile Ser Val Glu Thr Leu Gln Arg Leu Arg Asp Ala Lys Pro Gln Gly
 35 40 45

Gly Ile Gly Leu Leu Thr Val Lys Leu Asp Asp Pro Thr Gly Tyr Gly
 50 55 60

Arg Ile Thr Arg Glu Asn Gly Lys Val Thr Gly Ile Val Glu His Lys
 65 70 75 80

Asp Ala Thr Asp Glu Gln Arg Gln Ile Gln Glu Ile Asn Thr Gly Ile
 85 90 95

Leu Ile Ala Asn Gly Ala Asp Met Lys Arg Trp Leu Ala Lys Leu Thr
 100 105 110

Asn Asn Asn Ala Gln Gly Glu Tyr Tyr Ile Thr Asp Ile Ile Ala Leu
 115 120 125

Ala Tyr Gln Glu Gly Arg Glu Ile Val Ala Val His Pro Gln Arg Leu
 130 135 140

Ser Glu Val Glu Gly Val Asn Asn Arg Leu Gln Leu Ser Arg Leu Glu
 145 150 155 160

Arg Val Tyr Gln Ser Glu Gln Ala Glu Lys Leu Leu Leu Ala Gly Val
 165 170 175

Met Leu Arg Asp Pro Ala Arg Phe Asp Leu Arg Gly Thr Leu Thr His
 180 185 190

Gly Arg Asp Val Glu Ile Asp Thr Asn Val Ile Ile Glu Gly Asn Val
 195 200 205

Thr Leu Gly His Arg Val Lys Ile Gly Thr Gly Cys Val Ile Lys Asn
 210 215 220

Ser Val Ile Gly Asp Asp Cys Glu Ile Ser Pro Tyr Thr Val Val Glu
 225 230 235 240

Asp Ala Asn Leu Ala Ala Ala Cys Thr Ile Gly Pro Phe Ala Arg Leu
 245 250 255

Arg Pro Gly Ala Glu Leu Leu Glu Gly Ala His Val Gly Asn Phe Val
 260 265 270

Glu Met Lys Lys Ala Arg Leu Gly Lys Gly Ser Lys Ala Gly His Leu
 275 280 285

Thr Tyr Leu Gly Asp Ala Glu Ile Gly Asp Asn Val Asn Ile Gly Ala
290 295 300

Gly Thr Ile Thr Cys Asn Tyr Asp Gly Ala Asn Lys Phe Lys Thr Ile
305 310 315 320

Ile Gly Asp Asp Val Phe Val Gly Ser Asp Thr Gln Leu Val Ala Pro
325 330 335

Val Thr Val Gly Lys Gly Ala Thr Ile Ala Ala Gly Thr Thr Val Thr
340 345 350

Arg Asn Val Gly Glu Asn Ala Leu Ala Ile Ser Arg Val Pro Gln Thr
355 360 365

Gln Lys Glu Gly Trp Arg Arg Pro Val Lys Lys Lys
370 375 380

<210> 59
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 59
gatcgggtctc gcatgagtaa tcgtaaatat ttc

33

<210> 60
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 60
gatcctcgag tttaaagggt tttactgcat c

31

<210> 61
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 61
gatcgggtctc gcatgttgaa taatgctatg agc

33

<210> 62
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 62
gatcctcgag tcactttttc tttaccggac gac

33

<210> 63
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 63
gatggtctcg catggagcag ctgggtacgg gtc

33

<210> 64
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 64
gcgacgctct cccgggtgcg actcctgcat ta

32

<210> 65
<211> 46
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 65
gatctgtaca atccgatat agttcctcct ttcagcaaaa aacccc

46

<210> 66
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 66
gcgacgctct cccgggtgcg actcctgcat ta

32

<210> 67
 <211> 36
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 67
 gcgctaataca agttttcccg ggtcgagggtg ccgtaa 36

<210> 68
 <211> 35
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 68
 gatgcggccg cactgcagta attaccgcat ccaac 35

<210> 69
 <211> 34
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 69
 gatgtcgaca ccgattgatg cagcaaactg atcc 34

<210> 70
 <211> 32
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 70
 gatgcggccg cgcaaggcaa cagcaaactg gc 32

<210> 71
 <211> 42
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 71
 gatcgatcc tcaggctgtt accaaagaag ttgcaacctg gc 42

<210> 72
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 72
gatctgtaca agcaaccgca cctgtggc

28

<210> 73
<211> 46
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 73
gatcagcgct atccggatat agttcctcct ttcagcaaaa aacccc

46

<210> 74
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 74
gagcggccgc atgcaaaaatc ggctgaccat c

31

<210> 75
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 75
gatcgggccc ttacttctgt aaccaccaga cagcctc

37

<210> 76
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 76
gatcgggccc cttagccggg aaacgtctgg cggc

34

<210> 77
<211> 37
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 77
gatcgtcgac tcaggctttc acatcactca ctgcacc

37

<210> 78
<211> 27
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 78
gatggatcca gcaaccgcac ctgtggc

27

<210> 79
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 79
gatgcgatcg ctatagttcc tcctttcagc aaaaaaccc

39

<210> 80
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 80
agctgagctc atgtgtggaa ttgttggcgc ga

32

<210> 81
<211> 32
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 81
tacgaagctt actcaaccgt aaccgatttt gc

32

<210> 82
 <211> 34
 <212> DNA
 <213> Artificial sequence.

<220>
 <223> primer

<400> 82
 agctggtacc atgtgtggaa tcgtaggta tata

34

<210> 83
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 83
 tacgcatgct tactccacag taacactctt cgca

34

<210> 84
 <211> 382
 <212> PRT
 <213> Escherichia coli

<400> 84

Met Tyr Ala Leu Thr Gln Gly Arg Ile Phe Thr Gly His Glu Phe Leu
 1 5 10 15

Asp Asp His Ala Val Val Ile Ala Asp Gly Leu Ile Lys Ser Val Cys
 20 25 30

Pro Val Ala Glu Leu Pro Pro Glu Ile Glu Gln Arg Ser Leu Asn Gly
 35 40 45

Ala Ile Leu Ser Pro Gly Phe Ile Asp Val Gln Leu Asn Gly Cys Gly
 50 55 60

Gly Val Gln Phe Asn Asp Thr Ala Glu Ala Val Ser Val Glu Thr Leu
 65 70 75 80

Glu Ile Met Gln Lys Ala Asn Glu Lys Ser Gly Cys Thr Asn Tyr Leu
 85 90 95

Pro Thr Leu Ile Thr Thr Ser Asp Glu Leu Met Lys Gln Gly Val Arg
 100 105 110

Val Met Arg Glu Tyr Leu Ala Lys His Pro Asn Gln Ala Leu Gly Leu
 115 120 125

His Leu Glu Gly Pro Trp Leu Asn Leu Val Lys Lys Gly Thr His Asn
 130 135 140

Pro Asn Phe Val Arg Lys Pro Asp Ala Ala Leu Val Asp Phe Leu Cys
 145 150 155 160

Glu Asn Ala Asp Val Ile Thr Lys Val Thr Leu Ala Pro Glu Met Val
 165 170 175

Pro Ala Glu Val Ile Ser Lys Leu Ala Asn Ala Gly Ile Val Val Ser
 180 185 190

Ala Gly His Ser Asn Ala Thr Leu Lys Glu Ala Lys Ala Gly Phe Arg
 195 200 205

Ala Gly Ile Thr Phe Ala Thr His Leu Tyr Asn Ala Met Pro Tyr Ile
 210 215 220

Thr Gly Arg Glu Pro Gly Leu Ala Gly Ala Ile Leu Asp Glu Ala Asp
 225 230 235 240

Ile Tyr Cys Gly Ile Ile Ala Asp Gly Leu His Val Asp Tyr Ala Asn
 245 250 255

Ile Arg Asn Ala Lys Arg Leu Lys Gly Asp Lys Leu Cys Leu Val Thr
 260 265 270

Asp Ala Thr Ala Pro Ala Gly Ala Asn Ile Glu Gln Phe Ile Phe Ala
 275 280 285

Gly Lys Thr Ile Tyr Tyr Arg Asn Gly Leu Cys Val Asp Glu Asn Gly
 290 295 300

Thr Leu Ser Gly Ser Ser Leu Thr Met Ile Glu Gly Val Arg Asn Leu
 305 310 315 320

Val Glu His Cys Gly Ile Ala Leu Asp Glu Val Leu Arg Met Ala Thr
 325 330 335

Leu Tyr Pro Ala Arg Ala Ile Gly Val Glu Lys Arg Leu Gly Thr Leu
 340 345 350

Ala Ala Gly Lys Val Ala Asn Leu Thr Ala Phe Thr Pro Asp Phe Lys
 355 360 365

Ile Thr Lys Thr Ile Val Asn Gly Asn Glu Val Val Thr Gln
 370 375 380

<210> 85
 <211> 1149
 <212> DNA
 <213> Escherichia coli

<400> 85
 atgtatgcat taaccacagg ccgcatcttt accggccacg aatttcttga tgaccacgcg 60
 gttgttatcg ctgatggcct gattaaaagc gtctgtccgg tagcggaact gccgccagag 120
 atcgaacaac gttcactgaa cggggccatt ctctcccccg gttttatcga tgtgcagtta 180
 aacggctgcg gcggcgtaga gtttaacgac accgctgaag cggtcagcgt ggaaacgctg 240
 gaaatcatgc agaaagccaa tgagaaatca ggctgtacta actatctgcc gacgcttatc 300
 accaccagcg atgagctgat gaaacagggc gtgcgcgtta tgcgcgagta cctggcaaaa 360
 catccgaatc aggcgttagg tctgcatctg gaaggtccgt ggctgaatct ggtaaaaaaa 420
 ggcaccata atccgaattt tgtgcgtaag cctgatgccg cgctggtcga tttcctgtgt 480
 gaaaacgccg acgtcattac caaagtgacc ctggcaccgg aaatggttcc tgcggaagtc 540
 atcagcaaac tggcaaatgc cgggattgtg gtttctgccg gtcactccaa cgcgacgttg 600
 aaagaagcaa aagccggttt ccgcgcgggg attacctttg ccacccatct gtacaacgcg 660
 atgccgtata ttaccggtcg tgaacctggc ctggcggggc cgatcctcga cgaagctgac 720
 atttattgcg gtattattgc tgatggcctg catgttgatt acgccaacat tcgcaacgct 780
 aaacgtctga aaggcgacaa actgtgtctg gttactgacg ccaccgcgcc agcaggtgcc 840
 aacattgaac agttcatttt tgcgggtaaa acaatatact accgtaacgg actttgtgtg 900
 gatgagaacg gtacgttaag cggttcatcc ttaaccatga ttgaaggcgt gcgtaatctg 960
 gtcgaacatt gcggtatcgc actggatgaa gtgctacgta tggcgacgct ctatccggcg 1020
 cgtgcgattg gcgttgagaa acgtctcggc aactcgcgcg caggtaaagt agccaacctg 1080
 actgcattca cacctgattt taaaatcacc aagaccatcg ttaacggtaa cgaggtcgta 1140
 actcaataa 1149

<210> 86
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

 <400> 86
 gagcggccgc atgaatcaat cttatggacg gc 32

 <210> 87
 <211> 37
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 87
 gagtcgactc agcgtttgct gatctgatcg aacgtac 37

 <210> 88
 <211> 1410
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)..(1410)
 <223>

 <400> 88
 atg tcc gct gaa cac gta ctg acg atg ctg aac gag cac gaa gtg aag 48
 Met Ser Ala Glu His Val Leu Thr Met Leu Asn Glu His Glu Val Lys
 1 5 10 15

 ttt gtt gat ttg cgc ttc acc gat act aaa ggt aaa gaa cag cac gtc 96
 Phe Val Asp Leu Arg Phe Thr Asp Thr Lys Gly Lys Glu Gln His Val
 20 25 30

 act atc cct gct cat cag gtg aat gct gaa ttc ttc gaa gaa ggc aaa 144
 Thr Ile Pro Ala His Gln Val Asn Ala Glu Phe Phe Glu Glu Gly Lys
 35 40 45

 atg ttt gac ggc tcc tcg att ggc ggc tgg aaa ggc att aac gag tcc 192
 Met Phe Asp Gly Ser Ser Ile Gly Gly Trp Lys Gly Ile Asn Glu Ser
 50 55 60

 gac atg gtg ctg atg cca gac gca tcc acc gca gtg att gac ccg ttc 240
 Asp Met Val Leu Met Pro Asp Ala Ser Thr Ala Val Ile Asp Pro Phe
 65 70 75 80

 ttc gcc gac tcc acc ctg att atc cgt tgc gac atc ctt gaa cct ggc 288
 Phe Ala Asp Ser Thr Leu Ile Ile Arg Cys Asp Ile Leu Glu Pro Gly
 85 90 95

 acc ctg caa ggc tat gac cgt gac ccg cgc tcc att gcg aag cgc gcc 336
 Thr Leu Gln Gly Tyr Asp Arg Asp Pro Arg Ser Ile Ala Lys Arg Ala
 100 105 110

 gaa gat tac ctg cgt tcc act ggc att gcc gac acc gta ctg ttc ggg 384

Glu Asp Tyr Leu Arg Ser Thr Gly Ile Ala Asp Thr Val Leu Phe Gly	
115 120 125	
cca gaa cct gaa ttc ttc ctg ttc gat gac atc cgt ttc gga tca tct	432
Pro Glu Pro Glu Phe Phe Leu Phe Asp Asp Ile Arg Phe Gly Ser Ser	
130 135 140	
atc tcc ggt tcc cac gtt gct atc gac gat atc gaa ggc gca tgg aac	480
Ile Ser Gly Ser His Val Ala Ile Asp Asp Ile Glu Gly Ala Trp Asn	
145 150 155 160	
tcc tcc acc caa tac gaa ggt ggt aac aaa ggt cac cgt ccg gca gtg	528
Ser Ser Thr Gln Tyr Glu Gly Gly Asn Lys Gly His Arg Pro Ala Val	
165 170 175	
aaa ggc ggt tac ttc ccg gtt cca ccg gta gac tcg gct cag gat att	576
Lys Gly Gly Tyr Phe Pro Val Pro Pro Val Asp Ser Ala Gln Asp Ile	
180 185 190	
cgt tct gaa atg tgt ctg gtg atg gaa cag atg ggt ctg gtg gtt gaa	624
Arg Ser Glu Met Cys Leu Val Met Glu Gln Met Gly Leu Val Val Glu	
195 200 205	
gcc cat cac cac gaa gta gcg act gct ggt cag aac gaa gtg gct acc	672
Ala His His His Glu Val Ala Thr Ala Gly Gln Asn Glu Val Ala Thr	
210 215 220	
cgc ttc aat acc atg acc aaa aaa gct gac gaa att cag atc tac aaa	720
Arg Phe Asn Thr Met Thr Lys Lys Ala Asp Glu Ile Gln Ile Tyr Lys	
225 230 235 240	
tat gtt gtg cac aac gta gcg cac cgc ttc ggt aaa acc gcg acc ttt	768
Tyr Val Val His Asn Val Ala His Arg Phe Gly Lys Thr Ala Thr Phe	
245 250 255	
atg cca aaa ccg atg ttc ggt gat aac ggc tcc ggt atg cac tgc cac	816
Met Pro Lys Pro Met Phe Gly Asp Asn Gly Ser Gly Met His Cys His	
260 265 270	
atg tct ctg tct aaa aac ggc gtt aac ctg ttc gca ggc gac aaa tac	864
Met Ser Leu Ser Lys Asn Gly Val Asn Leu Phe Ala Gly Asp Lys Tyr	
275 280 285	
gca ggt ctg tct gag cag gcg ctg tac tac att ggc ggc gta atc aaa	912
Ala Gly Leu Ser Glu Gln Ala Leu Tyr Tyr Ile Gly Gly Val Ile Lys	
290 295 300	
cac gct aaa gcg att aac gcc ctg gca aac ccg acc acc aac tct tat	960
His Ala Lys Ala Ile Asn Ala Leu Ala Asn Pro Thr Thr Asn Ser Tyr	
305 310 315 320	
aag cgt ctg gtc ccg ggc tat gaa gca ccg gta atg ctg gct tac tct	1008
Lys Arg Leu Val Pro Gly Tyr Glu Ala Pro Val Met Leu Ala Tyr Ser	
325 330 335	
gcg cgt aac cgt tct gcg tct atc cgt att ccg gtg gtt tct tct ccg	1056
Ala Arg Asn Arg Ser Ala Ser Ile Arg Ile Pro Val Val Ser Ser Pro	
340 345 350	

aaa gca cgt cgt atc gaa gta cgt ttc ccg gat ccg gca gct aac ccg 1104
 Lys Ala Arg Arg Ile Glu Val Arg Phe Pro Asp Pro Ala Ala Asn Pro
 355 360 365

tac ctg tgc ttt gct gcc ctg ctg atg gcc ggt ctt gat ggt atc aag 1152
 Tyr Leu Cys Phe Ala Ala Leu Leu Met Ala Gly Leu Asp Gly Ile Lys
 370 375 380

aac aag atc cat ccg ggc gaa gcc atg gac aaa aac ctg tat gac ctg 1200
 Asn Lys Ile His Pro Gly Glu Ala Met Asp Lys Asn Leu Tyr Asp Leu
 385 390 395 400

ccg cca gaa gaa gcg aaa gag atc cca cag gtt gca ggc tct ctg gaa 1248
 Pro Pro Glu Glu Ala Lys Glu Ile Pro Gln Val Ala Gly Ser Leu Glu
 405 410 415

gaa gca ctg aac gaa ctg gat ctg gac cgc gag ttc ctg aaa gcc ggt 1296
 Glu Ala Leu Asn Glu Leu Asp Leu Asp Arg Glu Phe Leu Lys Ala Gly
 420 425 430

ggc gtg ttc act gac gaa gca att gat gcg tac atc gct ctg cgt cgc 1344
 Gly Val Phe Thr Asp Glu Ala Ile Asp Ala Tyr Ile Ala Leu Arg Arg
 435 440 445

gaa gaa gat gac cgc gtg cgt atg act ccg cat ccg gta gag ttt gag 1392
 Glu Glu Asp Asp Arg Val Arg Met Thr Pro His Pro Val Glu Phe Glu
 450 455 460

ctg tac tac agc gtc taa 1410
 Leu Tyr Tyr Ser Val
 465

<210> 89

<211> 469

<212> PRT

<213> Escherichia coli

<400> 89

Met Ser Ala Glu His Val Leu Thr Met Leu Asn Glu His Glu Val Lys
 1 5 10 15

Phe Val Asp Leu Arg Phe Thr Asp Thr Lys Gly Lys Glu Gln His Val
 20 25 30

Thr Ile Pro Ala His Gln Val Asn Ala Glu Phe Phe Glu Glu Gly Lys
 35 40 45

Met Phe Asp Gly Ser Ser Ile Gly Gly Trp Lys Gly Ile Asn Glu Ser
 50 55 60

Asp Met Val Leu Met Pro Asp Ala Ser Thr Ala Val Ile Asp Pro Phe
 65 70 75 80

Phe Ala Asp Ser Thr Leu Ile Ile Arg Cys Asp Ile Leu Glu Pro Gly
 85 90 95

Thr Leu Gln Gly Tyr Asp Arg Asp Pro Arg Ser Ile Ala Lys Arg Ala
 100 105 110

Glu Asp Tyr Leu Arg Ser Thr Gly Ile Ala Asp Thr Val Leu Phe Gly
 115 120 125

Pro Glu Pro Glu Phe Phe Leu Phe Asp Asp Ile Arg Phe Gly Ser Ser
 130 135 140

Ile Ser Gly Ser His Val Ala Ile Asp Asp Ile Glu Gly Ala Trp Asn
 145 150 155 160

Ser Ser Thr Gln Tyr Glu Gly Gly Asn Lys Gly His Arg Pro Ala Val
 165 170 175

Lys Gly Gly Tyr Phe Pro Val Pro Pro Val Asp Ser Ala Gln Asp Ile
 180 185 190

Arg Ser Glu Met Cys Leu Val Met Glu Gln Met Gly Leu Val Val Glu
 195 200 205

Ala His His His Glu Val Ala Thr Ala Gly Gln Asn Glu Val Ala Thr
 210 215 220

Arg Phe Asn Thr Met Thr Lys Lys Ala Asp Glu Ile Gln Ile Tyr Lys
 225 230 235 240

Tyr Val Val His Asn Val Ala His Arg Phe Gly Lys Thr Ala Thr Phe
 245 250 255

Met Pro Lys Pro Met Phe Gly Asp Asn Gly Ser Gly Met His Cys His
 260 265 270

Met Ser Leu Ser Lys Asn Gly Val Asn Leu Phe Ala Gly Asp Lys Tyr
 275 280 285

Ala Gly Leu Ser Glu Gln Ala Leu Tyr Tyr Ile Gly Gly Val Ile Lys
 290 295 300

His Ala Lys Ala Ile Asn Ala Leu Ala Asn Pro Thr Thr Asn Ser Tyr
 305 310 315 320

Lys Arg Leu Val Pro Gly Tyr Glu Ala Pro Val Met Leu Ala Tyr Ser
325 330 335

Ala Arg Asn Arg Ser Ala Ser Ile Arg Ile Pro Val Val Ser Ser Pro
340 345 350

Lys Ala Arg Arg Ile Glu Val Arg Phe Pro Asp Pro Ala Ala Asn Pro
355 360 365

Tyr Leu Cys Phe Ala Ala Leu Leu Met Ala Gly Leu Asp Gly Ile Lys
370 375 380

Asn Lys Ile His Pro Gly Glu Ala Met Asp Lys Asn Leu Tyr Asp Leu
385 390 395 400

Pro Pro Glu Glu Ala Lys Glu Ile Pro Gln Val Ala Gly Ser Leu Glu
405 410 415

Glu Ala Leu Asn Glu Leu Asp Leu Asp Arg Glu Phe Leu Lys Ala Gly
420 425 430

Gly Val Phe Thr Asp Glu Ala Ile Asp Ala Tyr Ile Ala Leu Arg Arg
435 440 445

Glu Glu Asp Asp Arg Val Arg Met Thr Pro His Pro Val Glu Phe Glu
450 455 460

Leu Tyr Tyr Ser Val
465

<210> 90
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 90
gatcgggtctc gcatgtccgc tgaacacgta ctgac

35

<210> 91
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 91
 gatcctcgag ttagacgctg tagtacagct c 31

<210> 92
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 92
 gatcgccggc ttacatgctg tagcccagc 29

<210> 93
 <211> 32
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 93
 gatcctgcag tcatgctgct aataatctat cc 32

<210> 94
 <211> 1476
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1476)
 <223>

<400> 94
 atg gcg gta acg caa aca gcc cag gtc tgt gac ttg gtc att ttc ggc 48
 Met Ala Val Thr Gln Thr Ala Gln Val Cys Asp Leu Val Ile Phe Gly
 1 5 10 15

gcg aaa ggc gac ctt gcg cgt cgt aaa ttg ctg cct tcc ctg tat caa 96
 Ala Lys Gly Asp Leu Ala Arg Arg Lys Leu Leu Pro Ser Leu Tyr Gln
 20 25 30

ctg gaa aaa gcc ggt cag ctc aac ccg gac acc cgg att atc ggc gta 144
 Leu Glu Lys Ala Gly Gln Leu Asn Pro Asp Thr Arg Ile Ile Gly Val
 35 40 45

ggg cgt gct gac tgg gat aaa gcg gca tat acc aaa gtt gtc cgc gag 192
 Gly Arg Ala Asp Trp Asp Lys Ala Ala Tyr Thr Lys Val Val Arg Glu
 50 55 60

gcg ctc gaa act ttc atg aaa gaa acc att gat gaa ggt tta tgg gac 240
 Ala Leu Glu Thr Phe Met Lys Glu Thr Ile Asp Glu Gly Leu Trp Asp
 65 70 75 80

acc ctg agc gca cgt ctg gat ttt tgt aat ctc gat gtc aat gac act	288
Thr Leu Ser Ala Arg Leu Asp Phe Cys Asn Leu Asp Val Asn Asp Thr	
85 90 95	
gct gca ttc agc cgt ctc ggc gcg atg ctg gat caa aaa aat cgt atc	336
Ala Ala Phe Ser Arg Leu Gly Ala Met Leu Asp Gln Lys Asn Arg Ile	
100 105 110	
acc att aac tac ttt gcc atg ccg ccc agc act ttt ggc gca att tgc	384
Thr Ile Asn Tyr Phe Ala Met Pro Pro Ser Thr Phe Gly Ala Ile Cys	
115 120 125	
aaa ggg ctt ggc gag gca aaa ctg aat gct aaa ccg gca cgc gta gtc	432
Lys Gly Leu Gly Glu Ala Lys Leu Asn Ala Lys Pro Ala Arg Val Val	
130 135 140	
atg gag aaa ccg ctg ggg acg tcg ctg gcg acc tcg cag gaa atc aat	480
Met Glu Lys Pro Leu Gly Thr Ser Leu Ala Thr Ser Gln Glu Ile Asn	
145 150 155 160	
gat cag gtt ggc gaa tac ttc gag gag tgc cag gtt tac cgt atc gac	528
Asp Gln Val Gly Glu Tyr Phe Glu Glu Cys Gln Val Tyr Arg Ile Asp	
165 170 175	
cac tat ctt ggt aaa gaa acg gtg ctg aac ctg ttg gcg ctg cgt ttt	576
His Tyr Leu Gly Lys Glu Thr Val Leu Asn Leu Leu Ala Leu Arg Phe	
180 185 190	
gct aac tcc ctg ttt gtg aat aac tgg gac aat cgc acc att gat cat	624
Ala Asn Ser Leu Phe Val Asn Asn Trp Asp Asn Arg Thr Ile Asp His	
195 200 205	
gtt gag att acc gtg gca gaa gaa gtg ggg atc gaa ggg cgc tgg ggc	672
Val Glu Ile Thr Val Ala Glu Glu Val Gly Ile Glu Gly Arg Trp Gly	
210 215 220	
tat ttt gat aaa gcc ggt cag atg cgc gac atg atc cag aac cac ctg	720
Tyr Phe Asp Lys Ala Gly Gln Met Arg Asp Met Ile Gln Asn His Leu	
225 230 235 240	
ctg caa att ctt tgc atg att gcg atg tct ccg ccg tct gac ctg agc	768
Leu Gln Ile Leu Cys Met Ile Ala Met Ser Pro Pro Ser Asp Leu Ser	
245 250 255	
gca gac agc atc cgc gat gaa aaa gtg aaa gta ctg aag tct ctg cgc	816
Ala Asp Ser Ile Arg Asp Glu Lys Val Lys Val Leu Lys Ser Leu Arg	
260 265 270	
cgc atc gac cgc tcc aac gta cgc gaa aaa acc gta cgc ggg caa tat	864
Arg Ile Asp Arg Ser Asn Val Arg Glu Lys Thr Val Arg Gly Gln Tyr	
275 280 285	
act gcg ggc ttc gcc cag ggc aaa aaa gtg ccg gga tat ctg gaa gaa	912
Thr Ala Gly Phe Ala Gln Gly Lys Lys Val Pro Gly Tyr Leu Glu Glu	
290 295 300	
gag ggc gcg aac aag agc agc aat aca gaa acc ttc gtg gcg atc cgc	960
Glu Gly Ala Asn Lys Ser Ser Asn Thr Glu Thr Phe Val Ala Ile Arg	
305 310 315 320	

gtc gac att gat aac tgg cgc tgg gcc ggt gtg cca ttc tac ctg cgt	1008
Val Asp Ile Asp Asn Trp Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg	
325 330 335	
act ggt aaa cgt ctg ccg acc aaa tgt tct gaa gtc gtg gtc tat ttc	1056
Thr Gly Lys Arg Leu Pro Thr Lys Cys Ser Glu Val Val Val Tyr Phe	
340 345 350	
aaa aca cct gaa ctg aat ctg ttt aaa gag tgc tgg cag gat ctg ccg	1104
Lys Thr Pro Glu Leu Asn Leu Phe Lys Glu Ser Trp Gln Asp Leu Pro	
355 360 365	
cag aat aaa ctg act atc cgt ctg caa cct gat gaa ggc gtg gat atc	1152
Gln Asn Lys Leu Thr Ile Arg Leu Gln Pro Asp Glu Gly Val Asp Ile	
370 375 380	
cag gta ctg aat aaa gtt cct ggc ctt gac cac aaa cat aac ctg caa	1200
Gln Val Leu Asn Lys Val Pro Gly Leu Asp His Lys His Asn Leu Gln	
385 390 395 400	
atc acc aag ctg gat ctg agc tat tca gaa acc ttt aat cag acg cat	1248
Ile Thr Lys Leu Asp Leu Ser Tyr Ser Glu Thr Phe Asn Gln Thr His	
405 410 415	
ctg gcg gat gcc tat gaa cgt ttg ctg ctg gaa acc atg cgt ggt att	1296
Leu Ala Asp Ala Tyr Glu Arg Leu Leu Leu Glu Thr Met Arg Gly Ile	
420 425 430	
cag gca ctg ttt gta cgt cgc gat gaa gtg gaa gaa gcc tgg aaa tgg	1344
Gln Ala Leu Phe Val Arg Arg Asp Glu Val Glu Glu Ala Trp Lys Trp	
435 440 445	
gta gac tcc att act gag gcg tgg gcg atg gac aat gat gcg ccg aaa	1392
Val Asp Ser Ile Thr Glu Ala Trp Ala Met Asp Asn Asp Ala Pro Lys	
450 455 460	
ccg tat cag gcc gga acc tgg gga ccc gtt gcc tgc gtg gcg atg att	1440
Pro Tyr Gln Ala Gly Thr Trp Gly Pro Val Ala Ser Val Ala Met Ile	
465 470 475 480	
acc cgt gat ggt cgt tcc tgg aat gag ttt gag taa	1476
Thr Arg Asp Gly Arg Ser Trp Asn Glu Phe Glu	
485 490	

<210> 95
 <211> 491
 <212> PRT
 <213> Escherichia coli

<400> 95

Met Ala Val Thr Gln Thr Ala Gln Val Cys Asp Leu Val Ile Phe Gly
1 5 10 15
Ala Lys Gly Asp Leu Ala Arg Arg Lys Leu Leu Pro Ser Leu Tyr Gln
20 25 30

Leu Glu Lys Ala Gly Gln Leu Asn Pro Asp Thr Arg Ile Ile Gly Val
 35 40 45

Gly Arg Ala Asp Trp Asp Lys Ala Ala Tyr Thr Lys Val Val Arg Glu
 50 55 60

Ala Leu Glu Thr Phe Met Lys Glu Thr Ile Asp Glu Gly Leu Trp Asp
 65 70 75 80

Thr Leu Ser Ala Arg Leu Asp Phe Cys Asn Leu Asp Val Asn Asp Thr
 85 90 95

Ala Ala Phe Ser Arg Leu Gly Ala Met Leu Asp Gln Lys Asn Arg Ile
 100 105 110

Thr Ile Asn Tyr Phe Ala Met Pro Pro Ser Thr Phe Gly Ala Ile Cys
 115 120 125

Lys Gly Leu Gly Glu Ala Lys Leu Asn Ala Lys Pro Ala Arg Val Val
 130 135 140

Met Glu Lys Pro Leu Gly Thr Ser Leu Ala Thr Ser Gln Glu Ile Asn
 145 150 155 160

Asp Gln Val Gly Glu Tyr Phe Glu Glu Cys Gln Val Tyr Arg Ile Asp
 165 170 175

His Tyr Leu Gly Lys Glu Thr Val Leu Asn Leu Leu Ala Leu Arg Phe
 180 185 190

Ala Asn Ser Leu Phe Val Asn Asn Trp Asp Asn Arg Thr Ile Asp His
 195 200 205

Val Glu Ile Thr Val Ala Glu Glu Val Gly Ile Glu Gly Arg Trp Gly
 210 215 220

Tyr Phe Asp Lys Ala Gly Gln Met Arg Asp Met Ile Gln Asn His Leu
 225 230 235 240

Leu Gln Ile Leu Cys Met Ile Ala Met Ser Pro Pro Ser Asp Leu Ser
 245 250 255

Ala Asp Ser Ile Arg Asp Glu Lys Val Lys Val Leu Lys Ser Leu Arg
 260 265 270

Arg Ile Asp Arg Ser Asn Val Arg Glu Lys Thr Val Arg Gly Gln Tyr
275 280 285

Thr Ala Gly Phe Ala Gln Gly Lys Lys Val Pro Gly Tyr Leu Glu Glu
290 295 300

Glu Gly Ala Asn Lys Ser Ser Asn Thr Glu Thr Phe Val Ala Ile Arg
305 310 315 320

Val Asp Ile Asp Asn Trp Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg
325 330 335

Thr Gly Lys Arg Leu Pro Thr Lys Cys Ser Glu Val Val Val Tyr Phe
340 345 350

Lys Thr Pro Glu Leu Asn Leu Phe Lys Glu Ser Trp Gln Asp Leu Pro
355 360 365

Gln Asn Lys Leu Thr Ile Arg Leu Gln Pro Asp Glu Gly Val Asp Ile
370 375 380

Gln Val Leu Asn Lys Val Pro Gly Leu Asp His Lys His Asn Leu Gln
385 390 395 400

Ile Thr Lys Leu Asp Leu Ser Tyr Ser Glu Thr Phe Asn Gln Thr His
405 410 415

Leu Ala Asp Ala Tyr Glu Arg Leu Leu Leu Glu Thr Met Arg Gly Ile
420 425 430

Gln Ala Leu Phe Val Arg Arg Asp Glu Val Glu Glu Ala Trp Lys Trp
435 440 445

Val Asp Ser Ile Thr Glu Ala Trp Ala Met Asp Asn Asp Ala Pro Lys
450 455 460

Pro Tyr Gln Ala Gly Thr Trp Gly Pro Val Ala Ser Val Ala Met Ile
465 470 475 480

Thr Arg Asp Gly Arg Ser Trp Asn Glu Phe Glu
485 490

<210> 96
<211> 32
<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 96

gacggtctc gcatggcgt aacgcaaaca gc

32

<210> 97

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 97

gacctcgag ttactcaaac tcattccagg aacgacc

37

<210> 98

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 98

cgaatatcac gcggtgacca gttaaac

27

<210> 99

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 99

cacagtgtgc cgatgatttt gacc

24

<210> 100

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 100

gaccaatggc ctaatggagc aaccgcacct gtggc

35

<210> 101

<211> 46

<212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 101
 gatcagcgct atccggatat agttcctcct ttcagcaaaa aacccc 46

 <210> 102
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 102
 gatgctagct aaccggagct catagggc 28

 <210> 103
 <211> 32
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 103
 gatttcgaat gatcagtgtc agatttttac cc 32

 <210> 104
 <211> 1650
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 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)..(1650)
 <223>

 <400> 104
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 1 5 10 15

 aaa cac ttc gat gaa atg aaa gac gtt acg atc gcc gat ctt ttt gct 96
 Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
 20 25 30

 aaa gac ggc gat cgt ttt tct aag ttc tcc gca acc ttc gac gat cag 144
 Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
 35 40 45

 atg ctg gtg gat tac tcc aaa aac cgc atc act gaa gag acg ctg gcg 192
 Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala

50	55	60	
aaa tta cag gat ctg gcg Lys Leu Gln Asp Leu Ala 65 70	aaa gag tgc gat ctg gcg Lys Glu Cys Asp Leu Ala 75 80	ggc gcg att aag Gly Ala Ile Lys	240
tcg atg ttc tct ggc gag Ser Met Phe Ser Gly Glu 85	aag atc aac cgc act Lys Ile Asn Arg Thr 90	gaa aac cgc gcc gtg Glu Asn Arg Ala Val 95	288
ctg cac gta gcg ctg cgt Leu His Val Ala Leu Arg 100	aac cgt agc aat acc Asn Arg Ser Asn Thr 105	ccg att ttg gtt gat Pro Ile Leu Val Asp 110	336
ggc aaa gac gta atg ccg Gly Lys Asp Val Met Pro 115	gaa gtc aac gcg gtg Glu Val Asn Ala Val 120	ctg gag aag atg aaa Leu Glu Lys Met Lys 125	384
acc ttc tca gaa gcg att Thr Phe Ser Glu Ala Ile 130	att tcc ggt gag tgg Ile Ser Gly Glu Trp 135	aaa ggt tat acc ggc Lys Gly Tyr Thr Gly 140	432
aaa gca atc act gac gta Lys Ala Ile Thr Asp Val 145	gtg aac atc ggg atc Val Asn Ile Gly Ile 150	ggc ggt tct gac ctc Gly Gly Ser Asp Leu 155	480
ggc cca tac atg gtg acc Gly Pro Tyr Met Val Thr 165	gaa gct ctg cgt ccg Glu Ala Leu Arg Pro 170	tac aaa aac cac ctg Tyr Lys Asn His Leu 175	528
aac atg cac ttt gtt tct Asn Met His Phe Val Ser 180	aac gtc gat ggg act Asn Val Asp Gly Thr 185	cac atc gcg gaa gtg His Ile Ala Glu Val 190	576
ctg aaa aaa gta aac ccg Leu Lys Lys Val Asn Pro 195	gaa acc acg ctg ttc Glu Thr Thr Leu Phe 200	ttg gta gca tct aaa Leu Val Ala Ser Lys 205	624
acc ttc acc act cag gaa Thr Phe Thr Thr Gln Glu 210	act atg acc aac gcc Thr Met Thr Asn Ala 215	cat agc gcg cgt gac His Ser Ala Arg Asp 220	672
tgg ttc ctg aaa gcg gca Trp Phe Leu Lys Ala Ala 225	ggt gat gaa aaa cac Gly Asp Glu Lys His 230	ggt gca aaa cac ttt Val Ala Lys His Phe 235	720
gcg gcg ctt tcc acc aat Ala Ala Leu Ser Thr Asn 245	gcc aaa gcc gtt ggc Ala Lys Ala Val Gly 250	gag ttt ggt att gat Glu Phe Gly Ile Asp 255	768
act gcc aac atg ttc gag Thr Ala Asn Met Phe Glu 260	ttc tgg gac tgg gtt Phe Trp Asp Trp Val 265	ggc ggc cgt tac tct Gly Gly Arg Tyr Ser 270	816
ttg tgg tca gcg att ggc Leu Trp Ser Ala Ile Gly 275	ctg tcg att gtt ctc Leu Ser Ile Val Leu 280	tcc atc ggc ttt gat Ser Ile Gly Phe Asp 285	864
aac ttc gtt gaa ctg ctt Leu Trp Ser Ala Ile Gly 290	tcc ggc gca cac gcg Ser Thr Val Leu Val 295	atg gac aag cat ttc Glu Thr Val Leu Val 300	912

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe	
290 295 300	
tcc acc acg cct gcc gag aaa aac ctg cct gta ctg ctg gcg ctg att	960
Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile	
305 310 315 320	
ggc atc tgg tac aac aat ttc ttt ggt gcg gaa act gaa gcg att ctg	1008
Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu	
325 330 335	
ccg tat gac cag tat atg cac cgt ttc gcg gcg tac ttc cag cag ggc	1056
Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly	
340 345 350	
aat atg gag tcc aac ggt aag tat gtt gac cgt aac ggt aac gtt gtg	1104
Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val	
355 360 365	
gat tac cag act ggc ccg att atc tgg ggt gaa cca ggc act aac ggt	1152
Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly	
370 375 380	
cag cac gcg ttc tac cag ctg atc cac cag gga acc aaa atg gta ccg	1200
Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro	
385 390 395 400	
tgc gat ttc atc gct ccg gct atc acc cat aac ccg ctc tct gat cat	1248
Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His	
405 410 415	
cac cag aaa ctg ctg tct aac ttc ttc gcc cag acc gaa gcg ctg gcg	1296
His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala	
420 425 430	
ttt ggt aaa tcc cgc gaa gtg gtt gag cag gaa tat cgt gat cag ggt	1344
Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly	
435 440 445	
aaa gat ccg gca acg ctt gac tac gtg gtg ccg ttc aaa gta ttc gaa	1392
Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu	
450 455 460	
ggc aac cgc ccg acc aac tcc atc ctg ctg cgt gaa atc act ccg ttc	1440
Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe	
465 470 475 480	
agc ctg ggt gcg ttg att gcg ctg tat gag cac aaa atc ttt act cag	1488
Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln	
485 490 495	
ggc gtg atc ctg aac atc ttc acc ttc gac cag tgg ggc gtg gaa ctg	1536
Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu	
500 505 510	
ggc aaa cag ctg gcg aac cgt att ctg cca gag ctg aaa gat gat aaa	1584
Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys	
515 520 525	

gaa atc agc agc cac gat agc tcg acc aat ggt ctg att aac cgc tat 1632
 Glu Ile Ser Ser His Asp Ser Ser Thr Asn Gly Leu Ile Asn Arg Tyr
 530 535 540

aaa gcg tgg cgc ggt taa 1650
 Lys Ala Trp Arg Gly
 545

<210> 105
 <211> 549
 <212> PRT
 <213> Escherichia coli

<400> 105

Met Lys Asn Ile Asn Pro Thr Gln Thr Ala Ala Trp Gln Ala Leu Gln
 1 5 10 15

Lys His Phe Asp Glu Met Lys Asp Val Thr Ile Ala Asp Leu Phe Ala
 20 25 30

Lys Asp Gly Asp Arg Phe Ser Lys Phe Ser Ala Thr Phe Asp Asp Gln
 35 40 45

Met Leu Val Asp Tyr Ser Lys Asn Arg Ile Thr Glu Glu Thr Leu Ala
 50 55 60

Lys Leu Gln Asp Leu Ala Lys Glu Cys Asp Leu Ala Gly Ala Ile Lys
 65 70 75 80

Ser Met Phe Ser Gly Glu Lys Ile Asn Arg Thr Glu Asn Arg Ala Val
 85 90 95

Leu His Val Ala Leu Arg Asn Arg Ser Asn Thr Pro Ile Leu Val Asp
 100 105 110

Gly Lys Asp Val Met Pro Glu Val Asn Ala Val Leu Glu Lys Met Lys
 115 120 125

Thr Phe Ser Glu Ala Ile Ile Ser Gly Glu Trp Lys Gly Tyr Thr Gly
 130 135 140

Lys Ala Ile Thr Asp Val Val Asn Ile Gly Ile Gly Gly Ser Asp Leu
 145 150 155 160

Gly Pro Tyr Met Val Thr Glu Ala Leu Arg Pro Tyr Lys Asn His Leu
 165 170 175

Asn Met His Phe Val Ser Asn Val Asp Gly Thr His Ile Ala Glu Val
 180 185 190

Leu Lys Lys Val Asn Pro Glu Thr Thr Leu Phe Leu Val Ala Ser Lys
 195 200 205

Thr Phe Thr Thr Gln Glu Thr Met Thr Asn Ala His Ser Ala Arg Asp
 210 215 220

Trp Phe Leu Lys Ala Ala Gly Asp Glu Lys His Val Ala Lys His Phe
 225 230 235 240

Ala Ala Leu Ser Thr Asn Ala Lys Ala Val Gly Glu Phe Gly Ile Asp
 245 250 255

Thr Ala Asn Met Phe Glu Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser
 260 265 270

Leu Trp Ser Ala Ile Gly Leu Ser Ile Val Leu Ser Ile Gly Phe Asp
 275 280 285

Asn Phe Val Glu Leu Leu Ser Gly Ala His Ala Met Asp Lys His Phe
 290 295 300

Ser Thr Thr Pro Ala Glu Lys Asn Leu Pro Val Leu Leu Ala Leu Ile
 305 310 315 320

Gly Ile Trp Tyr Asn Asn Phe Phe Gly Ala Glu Thr Glu Ala Ile Leu
 325 330 335

Pro Tyr Asp Gln Tyr Met His Arg Phe Ala Ala Tyr Phe Gln Gln Gly
 340 345 350

Asn Met Glu Ser Asn Gly Lys Tyr Val Asp Arg Asn Gly Asn Val Val
 355 360 365

Asp Tyr Gln Thr Gly Pro Ile Ile Trp Gly Glu Pro Gly Thr Asn Gly
 370 375 380

Gln His Ala Phe Tyr Gln Leu Ile His Gln Gly Thr Lys Met Val Pro
 385 390 395 400

Cys Asp Phe Ile Ala Pro Ala Ile Thr His Asn Pro Leu Ser Asp His
 405 410 415

His Gln Lys Leu Leu Ser Asn Phe Phe Ala Gln Thr Glu Ala Leu Ala
420 425 430

Phe Gly Lys Ser Arg Glu Val Val Glu Gln Glu Tyr Arg Asp Gln Gly
435 440 445

Lys Asp Pro Ala Thr Leu Asp Tyr Val Val Pro Phe Lys Val Phe Glu
450 455 460

Gly Asn Arg Pro Thr Asn Ser Ile Leu Leu Arg Glu Ile Thr Pro Phe
465 470 475 480

Ser Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Lys Ile Phe Thr Gln
485 490 495

Gly Val Ile Leu Asn Ile Phe Thr Phe Asp Gln Trp Gly Val Glu Leu
500 505 510

Gly Lys Gln Leu Ala Asn Arg Ile Leu Pro Glu Leu Lys Asp Asp Lys
515 520 525

Glu Ile Ser Ser His Asp Ser Ser Thr Asn Gly Leu Ile Asn Arg Tyr
530 535 540

Lys Ala Trp Arg Gly
545

<210> 106
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 106
gatcgggtctc gcatgaaaaa catcaatcca acgcagac

38

<210> 107
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 107
gatcctcgag ttaaccgcgc cagcgtttat agc

33

<210> 108
 <211> 31
 <212> DNA
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 <220>
 <223> primer

 <400> 108
 ggatcctacc tgacgctttt tatcgcaact c 31

<210> 109
 <211> 24
 <212> DNA
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 <220>
 <223> primer

 <400> 109
 cggacgcaca tcggcctcgt agac 24

<210> 110
 <211> 27
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 110
 gattccggaa gcaaccgcac ctgtggc 27

<210> 111
 <211> 39
 <212> DNA
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 <220>
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 <400> 111
 gatcacctgg ttatagttcc tcctttcagc aaaaaaccc 39

<210> 112
 <211> 24
 <212> DNA
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 <220>
 <223> primer

 <400> 112
 ggtcatccg gatacagtac gcga 24

<210> 113
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 113
ataaaccagc cgggcaaatg g

21

<210> 114
<211> 17
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 114
cgccaagctt ggtaccg

17

<210> 115
<211> 21
<212> DNA
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<220>
<223> primer

<400> 115
ccctctagat gcatgctcga g

21

<210> 116
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 116
attgtgcgct cagtatagga agg

23

<210> 117
<211> 19
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 117
cgatactgac gggctccag

19

<210> 118
 <211> 35
 <212> DNA
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 <220>
 <223> primer

 <400> 118
 gcaaaacctt tcgcggtcac ccatgatagc gcccg 35

<210> 119
 <211> 35
 <212> DNA
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 <220>
 <223> primer

 <400> 119
 cgggcgctat catgggtgac cgcgaaaggt ttgca 35

<210> 120
 <211> 30
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 120
 cacaggaaac acatatgacc atgattacgg 30

<210> 121
 <211> 23
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 121
 ccaccatgat attcggcaag cag 23

<210> 122
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> primer

 <400> 122
 cctttcgcgg tcaccagcaa a 21

<210> 123
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 123
ccgtaatcat ggtcatatgt gtttcctgtg

30

<210> 124
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 124
gacgaagcgg ccgcgtaaac g

21

<210> 125
<211> 41
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 125
cacacaggaa acagctatga ccatgattac ggattcactg g

41

<210> 126
<211> 41
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 126
ccagtgaatc cgtaatcatg gtcatactg tttcctgtgt g

41

<210> 127
<211> 30
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 127
gatcccggga acggacgatt agagatcacc

30

<210> 128.
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 128
gtcagagaag tcgttcttag cgatg

25

<210> 129
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 129
ggatctaaac ctcagtāgcg accggtcttag aactagtg

38

<210> 130
<211> 38
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 130
ccctcgcccc tctagagcat ttāaattcag tcaattac

38

<210> 131
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 131
cacgcaggca ggctttacct tcttc

25

<210> 132
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> primer

<400> 132
cggaagaaca agcgacggaa ggac

24

<210> 133
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 133
 cacgataaac ggtgaagcca tgtc

24

<210> 134
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> primer

<400> 134
 cgtccatttt cttgaacgct tcatccc

27

<210> 135
 <211> 698
 <212> DNA
 <213> Escherichia coli

<400> 135
 ccttttcgagg tcaccagcaa atcgcgctgt tagcggggccc attaatgttct gtctcggcgc 60
 gtctgcgtct ggctggctgg cataaatatc tctactcgcaa tcaaattcag ccgatagcgg 120
 aacgggaagg cgactggagt gccatgtccg gttttcaaca aacctgcaa atgctgaatg 180
 agggcatcgt tcccactgag atgctgggtg ccaacgatca gatggcgctg ggcgcaatgc 240
 gcgccattac cgagtccggg ctgcgcgttg gtgcggatat ctcggtagtg ggatacgacg 300
 ataccgaaga cagctcatgt tatatccgcg cggttaaccac catcaaacag gattttcgcc 360
 tgctggggca aaccagcgtg gaccgcttgc tgcaactctc tcagggccag gcggtgaagg 420
 gcaatcagct gttgcccgtc tctactggtga aaagaaaaac caccctggcg cccaatacgc 480
 aaaccgcctc tccccgcgag ttggccgatt cattaatgca gctggcacga caggtttccc 540
 gactggaaag cgggcagtga gcgcaacgca attaatgtga gttagctcac tcattaggca 600
 cccagggctt tacactttat gttccggct cgtatgttgt gtggaattgt gagcggataa 660
 caatttcaca caggaaacac atatgaccat gattacgg 698

<210> 136
 <211> 23
 <212> DNA
 <213> Artificial sequence

<220>

<223> primer

<400> 136

ggcggcttaa aatgtcctga atg

23

<210> 137

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<223> primer

<400> 137

cgaaatcatc gttgccagta actttacg

28